

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:42:12 ; Search time 60.37 Seconds
(without alignments)
15.917 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	75.4	274	2 B84930	H+-transporting ATP
2	38	66.7	65	2 S38469	hypothetical prote
3	38	66.7	408	2 C82178	conserved hypothet
4	38	66.7	478	2 T25899	hypothetical prote
5	38	66.7	996	2 F86410	protein F3M18.12 l
6	37	64.9	113	2 I38320	T-cell receptor be
7	37	64.9	196	2 AE2876	conserved hypothet
8	37	64.9	198	2 G97652	hypothetical prote
9	37	64.9	365	1 B64228	hypothetical prote
10	36	63.2	137	2 D58723	hypothetical prote
11	36	63.2	193	2 E65090	hypothetical 15.2
12	36	63.2	193	2 F85963	hypothetical prote
13	36	63.2	193	2 G91118	hypothetical prote
14	36	63.2	193	2 AF0889	conserved hypothet
15	36	63.2	288	2 G90368	hypothetical prote
16	36	63.2	383	2 JC2472	brain and reproduc
17	36	63.2	1054	2 S54473	TPS3 protein - yea
18	36	63.2	1070	2 S46755	hypothetical prote
19	35.5	62.3	83	1 W5WLHS	E5 protein - human
20	35	61.4	142	2 C82728	succinate dehydrog
21	35	61.4	224	2 G96527	protein F27J15.18
22	35	61.4	270	2 A34636	Fc-gamma receptor
23	35	61.4	299	2 S73406	hypothetical prote
24	35	61.4	316	2 S50336	NADH dehydrogenase
25	35	61.4	380	2 A83458	hypothetical prote
26	35	61.4	483	2 T03909	hypothetical prote
27	35	61.4	492	2 S74338	glycolate oxidase
28	35	61.4	577	2 T09024	proline-rich prote
29	35	61.4	612	2 T39684	hypothetical prote

30	35	61.4	974	2 A86263	Fl3K23.18 protein
31	35	61.4	1950	2 S12332	ubiquitin--protein
32	35	61.4	2103	1 JQ1621	genome polyprotein
33	34	59.6	80	2 AB0913	conserved hypothet
34	34	59.6	132	1 RWMS12	T-cell receptor ga
35	34	59.6	135	1 RWMSY1	T-cell receptor ga
36	34	59.6	137	2 E26420	T-cell receptor ga
37	34	59.6	138	2 G27639	T-cell receptor ga
38	34	59.6	138	2 A27639	T-cell receptor ga
39	34	59.6	138	2 D27639	T-cell receptor ga
40	34	59.6	139	2 F27639	T-cell receptor ga
41	34	59.6	139	2 B27639	T-cell receptor ga
42	34	59.6	139	2 C27639	T-cell receptor ga
43	34	59.6	139	2 E27639	T-cell receptor ga
44	34	59.6	156	2 AH1363	hypothetical prote
45	34	59.6	206	2 T25139	hypothetical prote

ALIGNMENTS

RESULT 1

B84930
H+-transporting ATP synthase (EC 3.6.1.34) A chain [imported] - Buchnera sp. (strain C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 24-Aug-2001
C;Accession: B84930
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
A;Reference number: A84930; MUID:20445173
A;Accession: B84930
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-274 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: atpB; BU002
C;Superfamily: H+-transporting ATP synthase protein 6
C;Keywords: hydrolase

Query Match 75.4%; Score 43; DB 2; Length 274;
Best Local Similarity 80.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
|||
Db 229 LLPWWTQCFL 238

RESULT 2

S38469
hypothetical protein D65 - Desulfurococcus mobilis (fragment)
C;Species: Desulfurococcus mobilis
C;Date: 13-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jul-2000
C;Accession: S54739; S38469
R;Ceccarelli, E.; Bocchetta, M.; Creti, R.; Sanangelantoni, A.M.; Tiboni, O.; Cammarara Mol. Gen. Genet. 246, 687-696, 1995
A;Title: Chromosomal organization and nucleotide sequence of the genes for elongation obilis.
A;Reference number: S54733; MUID:95206243
A;Accession: S54739
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-65 <CE2>
A;Cross-references: EMBL:X73582; NID:g410438; PIDN:CAAS1989.1; PID:g410444

Query Match 66.7%; Score 38; DB 2; Length 65;
Best Local Similarity 60.0%; Pred. No. 6.2;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | : | | |
Db 6 LTMWYARCFL 15

RESULT 3
C82178
conserved hypothetical protein VC1609 [imported] - Vibrio cholerae (strain N16961 serogr
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: C82178
R;Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
A;Accession: C82178
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-408 <HEI>
A;Cross-references: GB:AE004239; GB:AE003852; NID:g9656130; PIDN:AAF94763.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC1609
A;Map position: 1

Query Match 66.7%; Score 38; DB 2; Length 408;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMWITQCF 9
| : | : | | |
Db 345 LVWLAQCF 352

RESULT 4
T25899
hypothetical protein T20F7.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T25899
R;Miller, N.; Gattung, S.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid T20F7.
A;Reference number: Z20107
A;Accession: T25899
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-478 <MIL>
A;Cross-references: EMBL:U97550; PIDN:AAB52856.1; GSPDB:GN00028; CESP:T20F7.6
A;Experimental source: strain Bristol N2; clone T20F7
C;Genetics:
A;Gene: CESP:T20F7.6
A;Map position: X
A;Introns: 33/3; 112/2; 144/1; 205/3; 263/2; 300/3; 380/3; 402/2; 451/1

Query Match 66.7%; Score 38; DB 2; Length 478;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMWITQCF 9
| : | | | | |
Db 43 LLWINQCY 50

RESULT 5
F86410
protein F3M18.12 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: F86410
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: F86410
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-996 <STO>
A;Cross-references: GB:AE005172; NID:g6560764; PIDN:AAF16764.1; GSPDB:GN00141
C;Genetics:
A;Gene: F3M18.12
A;Map position: 1

Query Match 66.7%; Score 38; DB 2; Length 996;
Best Local Similarity 55.6%; Pred. No. 69;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMWITQCFL 10
: | | : | : | |
Db 209 VMWLTECHL 217

RESULT 6
I38320
T-cell receptor beta chain V region (V-beta 26, germline) precursor - human (fragment
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jan-2000
C;Accession: I38320
R;Slightom, J.L.; Siemieniak, D.R.; Sieu, L.C.; Koop, B.F.; Hood, L.
Genomics 20, 149-168, 1994
A;Title: Nucleotide sequence analysis of 77.7 kb of the human V beta T-cell receptor
A;Reference number: A54302; MUID:94292194
A;Accession: I38320
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-113 <RES>
A;Cross-references: EMBL:U03115; NID:g467918; PIDN:AAA17719.1; PID:g467929
C;Genetics:
A;Gene: TCRBV26S1
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F:35-113/Domain: immunoglobulin homology <IMM>

Query Match 64.9%; Score 37; DB 2; Length 113;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | : | | | |
Db 5 LLCWVTLCLL 14

RESULT 7
AE2876
conserved hypothetical protein Atu2439 [imported] - Agrobacterium tumefaciens (strain
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AE2876
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutayavin, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AE2876
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-196 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43427.1; PID:g17740928; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu2439
A;Map position: circular chromosome

Query Match 64.9%; Score 37; DB 2; Length 196;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
| | | | |
Db 24 LLMWVTPAF 32

RESULT 8
G97652
hypothetical protein AGR_C_4424 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: G97652
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; PMID:11743194
A;Accession: G97652
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-198 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK88176.1; PID:g15157620; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_4424
A;Map position: circular chromosome

Query Match 64.9%; Score 37; DB 2; Length 198;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
| | | | |
Db 26 LLMWVTPAF 34

RESULT 9
B64228
hypothetical protein MG255 - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999
C;Accession: B64228
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J. , C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346
A;Accession: B64228
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-365 <TIGR>
A;Cross-references: GB:U39703; GB:L43967; NID:g1045933; PID:g1045946; TIGR:MG255
A;Experimental source: strain G-37

C;Genetics:
A;Genetic code: SGC3
C;Superfamily: Mycoplasma hypothetical protein MG255

Query Match 64.9%; Score 37; DB 1; Length 365;
Best Local Similarity 55.6%; Pred. No. 43;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMWITQCFL 10
| | | | |
Db 117 LLWLRCWL 125

RESULT 10
D58723
hypothetical protein (orf4, cpdA 5' region) - Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 20-Feb-1998
C;Accession: D58723
R;Imamura, R.; Yamanaka, K.; Ogura, T.; Hiraga, S.; Fujita, N.; Ishihama, A.; Niki, H. J. Biol. Chem. 271, 25423-25429, 1996
A;Title: Identification of the cpdA gene encoding cyclic 3',5'-adenosine monophosphat
A;Reference number: A58723; MUID:96411758
A;Accession: D58723
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-137 <IMA>
A;Cross-references: GB:D16557; NID:g453393
A;Experimental source: strain K-12
C;Genetics:
A;Map position: 68.4 min

Query Match 63.2%; Score 36; DB 2; Length 137;
Best Local Similarity 57.1%; Pred. No. 27;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 WITQCFL 10
| | | | |
Db 77 WLSQCFM 83

RESULT 11
E65090
hypothetical 15.2 kD protein in icc 3' region - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C;Accession: E65090
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; .A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: E65090
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-193 <BLAT>
A;Cross-references: GB:AE000385; GB:U00096; NID:g1789405; PIDN:AAC76067.1; PID:g17894
A;Experimental source: strain K-12, substrain MGL655
C;Genetics:
A;Gene: yqiA

Query Match 63.2%; Score 36; DB 2; Length 193;
Best Local Similarity 57.1%; Pred. No. 37;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 WITQCFL 10
| | | | |
Db 77 WLSQCFM 83


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RESULT 12
F85963
hypothetical protein yqiA [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: F85963
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: F85963
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-193 <STO>
A;Cross-references: GB:AE005174; NID:g12517609; PIDN:AAG58170.1; GSPDB:GN00145; UWGP:243
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yqiA

Query Match      63.2%; Score 36; DB 2; Length 193;
Best Local Similarity 57.1%; Pred. No. 37;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 WITQCFL 10
      |:|:|:|:
Db      77 WLSQCFM 83

RESULT 13
G91118
hypothetical protein ECs3919 [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: G91118
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G91118
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-193 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37342.1; PID:g13363392; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: ECs3919

Query Match      63.2%; Score 36; DB 2; Length 193;
Best Local Similarity 57.1%; Pred. No. 37;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 WITQCFL 10
      |:|:|:|:
Db      77 WLSQCFM 83

RESULT 14
AF0889
conserved hypothetical protein STY3360 [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AF0889
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
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A;Reference number: AB0502; PMID:11677608
A;Accession: AF0889
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-193 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD03014.1; PID:g16504259; GSPDB:GN00176
C;Genetics:
A;Gene: STY33360

Query Match      63.2%; Score 36; DB 2; Length 193;
Best Local Similarity 57.1%; Pred. No. 37;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 WITQCFL 10
      |:|:|:|:
Db      77 WLSQCFM 83

RESULT 15
G90368
hypothetical protein acsA-4 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: G90368
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Ch
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: G90368
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-288 <KUR>
A;Cross-references: GB:AE006641; NID:g13815300; PIDN:AAK42206.1; GSPDB:GN00155
C;Genetics:
A;Gene: acsA-4

Query Match      63.2%; Score 36; DB 2; Length 288;
Best Local Similarity 55.6%; Pred. No. 52;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      2 LMWITQCFL 10
      |:|:|:|:|:
Db      280 LLYITQCYM 288

Search completed: July 16, 2002, 07:48:18
Job time: 366 sec
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Access DB# 10937

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
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Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

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Searcher Phone #: <u>211458</u>	AA Sequence (#) <u>✓</u>	Dialog _____
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Date Completed: <u>7/16/02</u>	Litigation _____	Lexis/Nexis <u>✓</u>
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
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Online Time: <u>10</u>	Other _____	Other (specify) _____

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Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

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 Date Completed: 11/3/02
 Searcher Prep & Review Time: 30
 Clerical Prep Time: 20
 Online Time: 20

Type of Search

NA Sequence (#) _____
 AA Sequence (#) 12
 Structure (#) _____
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 Fulltext _____
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STN _____
 Dialog _____
 Questel/Orbit _____
 Dr. Link _____
 Lexis/Nexis _____
 Sequence Systems ☒ _____
 WWW/Internet _____
 Other (specify) _____


```
SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

Query Match 100.0%; Score 57; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
   | | | | | | | |
Db 158 LLMWITQCFL 167

RESULT 2
ATP6_BUCAI STANDARD; PRT; 274 AA.
AC P57118;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ATP synthase A chain (EC 3.6.3.14) (Protein 6).
GN ATPB OR BU002.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TOKYO 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -!- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
CC DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE
CC (BY SIMILARITY).
CC -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
CC -----
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CC -----
DR EMBL; AP001118; BAB12730.1; -.
DR InterPro; IPR000568; ATP_synt_A.
DR Pfam; PF00119; ATP_synt_A; 1.
DR PRINTS; PR00123; ATPASEA.
DR PROSITE; PS00449; ATPASE_A; 1.
KW Hydrogen ion transport; CF(0); Transmembrane; Complete proteome.
FT TRANSMEM 44 64.
FT TRANSMEM 110 130
FT TRANSMEM 156 176
FT TRANSMEM 179 199
FT TRANSMEM 212 232
FT TRANSMEM 243 263
FT TRANSMEM 274 AA; 31363 MW; 4B2321336FEFE78A4 CRC64;
SQ SEQUENCE 274 AA; 31363 MW; 4B2321336FEFE78A4 CRC64;

Query Match 75.4%; Score 43; DB 1; Length 274;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
   | | | | | | | |
Db 229 LLPWWTQCFL 238
```

```
RESULT 3
Y255_MYCGE
ID Y255_MYCGE STANDARD; PRT; 365 AA.
AC P47497; Q49289; Q49297;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG255.
GN MG255.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Fritchman J.L., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Nguyen D.T., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA Tomb J.-F., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RA "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
RN [2]
RP SEQUENCE OF 134-365 FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
RT sequencing.";
RL J. Bacteriol. 175:7918-7930(1993).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----
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CC -----
DR EMBL; U39704; AAC71475.1; -.
DR EMBL; U02174; AAD12457.1; -.
DR EMBL; U02164; AAD12446.1; -.
DR TIGR; MG255; -.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 105 125
FT TRANSMEM 151 171
FT TRANSMEM 187 207
FT TRANSMEM 180 180
FT CONFLICT 180 180 N -> KR (IN REF. 2).
SQ SEQUENCE 365 AA; 42440 MW; 6609C2C8CA2CC5B7 CRC64;

Query Match 64.9%; Score 37; DB 1; Length 365;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMWITQCFL 10
   | : : | | : |
Db 117 LLWLRQCWL 125

RESULT 4
YQIA_ECOLI
ID YQIA_ECOLI STANDARD; PRT; 193 AA.
AC P36653;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
```

DE Hypothetical protein yqIA.
GN YQIA OR B3031 OR 24388 OR ECS3919.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [4]
RP SEQUENCE OF 1-137 FROM N.A.
RC STRAIN=K12;
RA Imamura R., Niki H., Yamanaka K., Ogura T., Fujita N., Ishihama A.,
RA Hiraga S.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; U28377; AAA69199.1; -.
DR EMBL; AE000385; AAC76067.1; -.
DR EMBL; AE005533; AAG58170.1; -.
DR EMBL; AP002564; BAB37342.1; -.
DR EMBL; D16557; -; NOT_ANNOTATED_CDS.
DR EcoGene; EG12186; yqIA.
DR InterPro; IPR000379; Est_lip_thioest_actsite.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 135 137 APD -> GRI (IN REF. 4).
SQ SEQUENCE 193 AA; 21641 MW; 3077DED58BC0E8A3 CRC64;

Query Match 63.2%; Score 36; DB 1; Length 193;
Best Local Similarity 57.1%; Pred. No. 17;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 WITQCEL 10
|::|||:

Db 77 WLSQCFM 83

RESULT 5
VOD1_ARATH
ID VOD1_ARATH STANDARD; PRT; 351 AA.
AC Q9LJI5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable vacuolar ATP synthase subunit d 1 (EC 3.6.3.14) (V-ATPase d
DE subunit 1) (Vacuolar proton pump d subunit 1).
GN AT3G28710 OR MZN14.21.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansonge W., Unseld M.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisine N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erflie H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bagues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Lilauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana.";
RL Nature 408:820-822(2000).
CC -!- FUNCTION: SUBUNIT OF THE INTEGRAL MEMBRANE V0 COMPLEX OF VACUOLAR
CC ATPASE. VACUOLAR ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF
CC INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS, THUS PROVIDING
CC MOST OF THE ENERGY REQUIRED FOR TRANSPORT PROCESSES IN THE
CC VACUOLAR SYSTEM.
CC -!- SUBUNIT: V-ATPase is an heteromultimeric enzyme composed of a
CC peripheral catalytic V1 complex (components A to H) attached to
CC an integral membrane V0 proton pore complex (components: a, c, c',
CC c'' and d).
CC -!- SIMILARITY: BELONGS TO THE V-ATPASE V0D/AC39 SUBUNIT FAMILY.
CC -----
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CC -----
CC EMBL; AP000420; BAB02186.1; -.
DR InterPro; IPR002843; vATP-synt_AC39.
DR Pfam; PF01992; vATP-synt_AC39; 1.
DR

KW Hydrolase; Hydrogen ion transport.
SQ SEQUENCE 351 AA; 40791 MW; 5E1A67A149AC4EF4 CRC64;

Query Match 63.2%; Score 36; DB 1; Length 351;
Best Local Similarity 71.4%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMWITQC 8
||||:|
Db 328 LMWISec 334

RESULT 6
V0D2_ARATH STANDARD; PRT; 351 AA.
AC Q9LHA4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable vacuolar ATP synthase subunit d 2 (EC 3.6.3.14) (V-ATPase d subunit 2) (Vacuolar proton pump d subunit 2).
GN AT3G28715 OR MZNI4.22.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.;
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisme N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Barges M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelde B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argirou A., Flores M., Liquori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis thaliana";
RL Nature 408:820-822(2000).
CC -!- FUNCTION: SUBUNIT OF THE INTEGRAL MEMBRANE V0 COMPLEX OF VACUOLAR ATPASE. VACUOLAR ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS, THUS PROVIDING MOST OF THE ENERGY REQUIRED FOR TRANSPORT PROCESSES IN THE VACUOLAR SYSTEM.
CC -!- SUBUNIT: V-ATPase is an heteromultimeric enzyme composed of a peripheral catalytic V1 complex (components A to H) attached to an integral membrane V0 proton pore complex (components: a, c, c', c'', and d).
CC -!-SIMILARITY: BELONGS TO THE V-ATPASE V0D/AC39 SUBUNIT FAMILY.
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CC -----
DR EMBL; AP002057; BAB03168.1; -
DR EMBL; AP000420; BAB03168.1; JOINED.
DR InterPro; IPR002843; VATP-synt_AC39.
DR Pfam; PF01992; VATP-synt_AC39; 1.
KW Hydrolase; Hydrogen ion transport.
SQ SEQUENCE 351 AA; 40787 MW; DEA55CA48329E544 CRC64;

Query Match 63.2%; Score 36; DB 1; Length 351;
Best Local Similarity 71.4%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMWITQC 8
||||:|
Db 328 LMWISec 334

RESULT 7
TPS3_YEAST STANDARD; PRT; 1022 AA.
AC P38426;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 115 kDa subunit
DE (EC 2.4.1.15) (Trehalose-6-phosphate synthase) (UDP-glucose-
DE glucosephosphate glucosyltransferase).
GN TPS3 OR YMR261C OR YM8156.03C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Manning A.M., Rosenbloom C.L., Beaudet A.L.;
RL Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Lye G., Churcher C.M., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-glucose 6-phosphate = UDP +
CC alpha,alpha-trehalose 6-phosphate.
CC -!- SUBUNIT: TREHALOSE SYNTHASE/PHOSPHATASE COMPLEX CONTAINS THREE
CC OR FOUR POLYPEPTIDES OF 56 kDa (TPS1), 102 kDa (TPS2), 115 kDa
CC (TPS3) AND 123 kDa (TSL1).
CC -!- INDUCTION: REPRESSED BY GLUCOSE.
CC -!- SIMILARITY: CONTAINS A DOMAIN FOUND IN ALL THE PROTEINS OF THE
CC TPS COMPLEX.
CC -----
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CC -----
DR EMBL; M88172; AAA35224.1; ALT_INIT.
DR EMBL; Z49260; CAA89244.1; ALT_INIT.
DR SGD; S0004874; TPS3.
DR InterPro; IPR001830; Glyco_transf_20.
DR InterPro; IPR003337; Trehalose_PPase.
DR Pfam; PF00982; Glyco_transf_20; 1.
DR Pfam; PF02358; Trehalose_PPase; 1.
KW transferase; Glucosyltransferase; Glycolysis.


```
FT DOMAIN 255 746 TPS COMPLEX DOMAIN.
FT CONFLICT 154 154 P -> L (IN REF. 1).
FT CONFLICT 733 733 N -> D (IN REF. 1).
FT CONFLICT 802 802 S -> G (IN REF. 1).
FT CONFLICT 870 870 D -> E (IN REF. 1).
SQ SEQUENCE 1022 AA; 115363 MW; 49AD0A9E194E5962 CRC64;

Query Match 63.2%; Score 36; DB 1; Length 1022;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 WITQCF 9
|||:|
Db 723 WITKCF 728

RESULT 8
YHV4_YEAST STANDARD; PRT; 1070 AA.
AC P38850;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 123.0 kDa protein in SPO16-REC104 intergenic region.
GN YHR154W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
VIII."
RL Science 265:2077-2082(1994).
CC -1- SIMILARITY: CONTAINS 2 BRCT DOMAINS.
-----
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-----
DR EMBL; U10397; AAB68978.1; -.
DR PIR; S46755; S46755.
DR SGD; S0001197; ESC4.
DR InterPro; IPR001357; BRCT.
DR Pfam; PF00533; BRCT; 5.
DR SMART; SM00292; BRCT; 4.
DR PROSITE; PS50172; BRCT; 2.
KW Hypothetical protein; Repeat.
FT DOMAIN 117 210 BRCT 1.
FT DOMAIN 370 466 BRCT 2.
SQ SEQUENCE 1070 AA; 123017 MW; 767931285BB52580 CRC64;

Query Match 63.2%; Score 36; DB 1; Length 1070;
Best Local Similarity 50.0%; Pred. No. 81;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 MWITQCF 10
||: ||:
```

```
Db 447 MWLEQCYM 454

RESULT 9
VE5_HPV16
ID VE5_HPV16 STANDARD; PRT; 83 AA.
AC P06927;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Probable E5 protein.
GN E5.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88160059; PubMed=2831662;
RA Bubb V., McCance D.J., Schlegel R.;
RT "DNA sequence of the HPV-16 E5 ORF and the structural conservation of
its encoded protein.";
RL Virology 163:243-246(1988).
RN [2]
RP SEQUENCE OF 20-83 FROM N.A.
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185(1985).
CC -----
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-----
DR EMBL; K02718; AAA46938.1; ALT_SEQ.
DR PIR; A30016; W5WLHS.
DR InterPro; IPR004270; Papilloma_E5.
DR Pfam; PF03025; Papilloma_E5; 1.
KW Early protein.
SQ SEQUENCE 83 AA; 9401 MW; 442C0ABF0D77CDCF CRC64;

Query Match 62.3%; Score 35.5; DB 1; Length 83;
Best Local Similarity 46.7%; Pred. No. 9.2;
Matches 7; Conservative 3; Mismatches 0; Indels 5; Gaps 1;

QY 1 LLMWIT-----QCFL 10
||:| | | :| |
Db 47 LLLWITAASAFRCFI 61

RESULT 10
Y060_MYCPN STANDARD; PRT; 299 AA.
ID Y060_MYCPN
AC P75042;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative glycosyl transferase MG060 homolog (EC 2.-.-.-)
DE (D09 orf299).
GN MPN075 OR MP080.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
```

```
RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996)
CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
CC STRONG, TO M.GENITALIUM MG060.
CC -----
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CC -----
CC EMBL; AE000010; AAB95728.1; -.
DR InterPro; IPR001173; Glycos_transf_2.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Hypothetical protein; Transferase; Glycosyltransferase;
KW Complete proteome.
SQ SEQUENCE 299 AA; 35079 MW; 6E3F89EDAE420417 CRC64;

Query Match 61.4%; Score 35; DB 1; Length 299;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 WITQCFL 10
Db 274 WYTRCFL 280

RESULT 11
FCG2_CAVPO STANDARD; PRT; 341 AA.
AC Q60513; Q60512; Q60511; Q60498;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Low affinity immunoglobulin gamma FC region receptor II precursor (FC-
DE gamma RII) (FCRII) (IGG FC receptor II) (FC-gamma-1/gamma-2 receptor).
GN FCGR2.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2R-B1).
RX MEDLINE=90241239; PubMed=1692213;
RA Tominaga M., Sakata A., Ohmura T., Yamashita T., Koyama J., Onoue K.;
RT "The structure and expression of the guinea pig Fc receptor for IgG1
RT and IgG2 (Fc gamma 1/gamma 2R).";
RL Biochem. Biophys. Res. Commun. 168:683-689(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 2R-B1; 2R-B2 AND 2R-B3).
RX STRAIN=JY-1;
RX MEDLINE=93346746; PubMed=8345193;
RA Yamashita T., Shinohara K., Yamashita Y.;
RT "Expression cloning of complementary DNA encoding three distinct
RT isoforms of guinea pig Fc receptor for IgG1 and IgG2.";
RL J. Immunol. 151:2014-2023(1993).
CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS GAMMA. LOW
CC AFFINITY RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 2R-B1, 2R-B2 AND 2R-B3 (SHOWN
CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: MACROPHAGES AND POLYMORPHONUCLEAR LEUKOCYTES
CC EXPRESS PREFERENTIALLY 2R-B1. B LYMPHOCYTES EXPRESS ALL THREE
CC FORMS.
CC -!- DOMAIN: CONTAINS AN INTRACYTOPLASMIC MOTIF REFERRED AS
CC IMMUNORECEPTOR TYROSINE-BASED INHIBITOR MOTIF (ITIM). THIS MOTIF
CC IS INVOLVED IN DOWNMODULATION OF CELLULAR FUNCTIONS.
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CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
CC EMBL; D13693; BAA02852.1; -.
DR EMBL; D13692; BAA02851.1; -.
DR EMBL; D13691; BAA02850.1; -.
DR EMBL; M35272; AAA37036.1; ALT_INIT.
DR HSSP; P12319; IALT.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_like; 1.
KW IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat; Alternative splicing.
FT SIGNAL 1 42 POTENTIAL.
FT CHAIN 43 341 LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
FT REGION RECEPTOR II.
FT DOMAIN 43 224 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 225 245 POTENTIAL.
FT DOMAIN 246 341 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 64 120 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 145 203 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 318 323 ITIM MOTIF.
FT DISULFID 71 113 BY SIMILARITY.
FT DISULFID 152 196 BY SIMILARITY.
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 273 301 GEYSVVFSGSMSCPLDGLDPARTDLS -> A (IN
FT VARSPLIC 257 301 ISOFORM 2R-B2).
FT VARSPLIC 301 GNPEHREMGETLPEDPGEYSVVFSGSMSCPLDGLDPAR
FT CONFLICT 114 114 TDLS -> A (IN ISOFORM 2R-B1).
FT SEQUENCE 341 AA; 37091 MW; 5137E3271D443B84 CRC64;
SQ

Query Match 61.4%; Score 35; DB 1; Length 341;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 28 MLLWITVLF 37

RESULT 12
UBR1_YEAST
ID UBR1_YEAST STANDARD; PRT; 1950 AA.
AC P19812;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE N-end-recognizing protein (Ubiquitin-protein ligase E3 component) (N-
DE recognin).
GN UBR1 OR PTR1 OR YGR184C OR G7168.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
```



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RC STRAIN=S288C / GRF88;
RX MEDLINE=91006011; PubMed=2209542;
RA Bartel B.A., Wuening I., Varshavsky A.;
RT "The recognition component of the N-end rule pathway.";
RL EMBO J. 9:3179-3189(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=97279231; PubMed=9133739;
RA Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez-Perez M.,
RA Nombela C.;
RT "DNA sequence analysis of a 23,002 bp DNA fragment of the right arm
RT of Saccharomyces cerevisiae chromosome VII.";
RL Yeast 13:357-363(1997).
RN [3]
RP SEQUENCE OF 346-1950 FROM N.A.
RA Hebling U., Hofmann B., Delius H.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECOGNITION COMPONENT OF THE N-END RULE PATHWAY. BINDS
CC TO PROTEINS BEARING AMINO-TERMINAL RESIDUES THAT ARE DESTABILIZING
CC ACCORDING TO THE N-END RULE, BUT DOES NOT BIND TO OTHERWISE
CC IDENTICAL PROTEINS BEARING STABILIZING AMINO-TERMINAL RESIDUES.
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CC -----
CC DR EMBL; X53747; CAA37779.1; -.
CC DR EMBL; X99074; CAA67528.1; -.
CC DR EMBL; Z72969; CAA97210.1; -.
CC DR PIR; S12332; S12332.
CC DR SGD; S0003416; UBR1.
CC DR InterPro; IPR003126; Znf_UBR1.
CC DR InterPro; IPR001841; Znf_ring.
CC DR Pfam; PF02207; zf-UBR1; 1.
CC DR SMART; SM00184; RING; 1.
CC DR SMART; SM00396; Znf_UBR1; 1.
KW Ligase; Ubiquitin conjugation.
SQ SEQUENCE 1950 AA; 224836 MW; 33E4CD3A031AF523 CRC64;

Query Match 61.4%; Score 35; DB 1; Length 1950;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
DB 395 IILWITHC 402

RESULT 13
RRPL_UUK
ID RRPL_UUK STANDARD; PRT; 2103 AA.
AC P33453;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RNA-directed RNA polymerase (EC 2.7.7.48) (L protein).
GN L.
OS Uukuniemi virus (Uuk).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S23;
RX MEDLINE=92333259; PubMed=1629699;
RA Elliott R.M., Dunn E., Simons J.F., Pettersson R.F.;
RT "Nucleotide sequence and coding strategy of the Uukuniemi virus L RNA
RT segment.";
```

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RL J. Gen. Virol. 73:1745-1752(1992).
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
CC -----
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CC -----
CC DR EMBL; D10759; BAA01590.1; -.
CC DR PIR; JQ1621; JQ1621.
KW Transferase; Nucleotidyltransferase; RNA-directed RNA polymerase.
SQ SEQUENCE 2103 AA; 241039 MW; B0EA708451B0B6BD CRC64;

Query Match 61.4%; Score 35; DB 1; Length 2103;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
DB 1207 LLRWITAC 1214

RESULT 14
TVC3_MOUSE
ID TVC3_MOUSE STANDARD; PRT; 132 AA.
AC P06324;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE T-cell receptor gamma chain V region DFL12 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85137888; PubMed=3871915;
RA Kranz D.M., Saito H., Heller M., Takagaki Y., Haas W., Eisen H.N.,
RA Tonegawa S.;
RT "Limited diversity of the rearranged T-cell gamma gene.";
RL Nature 313:752-755(1985).
DR PIR; A02019; RWMS12.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW T-cell; Receptor; Signal.
FT SIGNAL 1
FT CHAIN 19 132 T-CELL RECEPTOR GAMMA CHAIN V REGION
FT DFL12.
FT DOMAIN 19 114 V SEGMENT.
FT DOMAIN 115 132 J SEGMENT.
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 15434 MW; 855D714D04A3CCFE CRC64;

Query Match 59.6%; Score 34; DB 1; Length 132;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
DB 3 LLRWFTSCCL 12

RESULT 15
TVC1_MOUSE
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ID TVCL_MOUSE STANDARD; PRT; 135 AA.
AC P01740;
DT 21-JUL-1986 (Rel. 01, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE T-cell receptor gamma chain V region V108A precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099339; PubMed=3917858;
RA Hayday A.C., Saito H., Gillies S.D., Kranz D.M., Tanigawa G.,
RA Eisen H.N., Tonegawa S.;
RT "Structure, organization, and somatic rearrangement of T cell gamma
RT genes."
RL Cell 40:259-269(1985).
RN [2]
RP SEQUENCE FROM N.A. (CLONE PHDS4/PHDS203).
RC STRAIN=BALB.B;
RX MEDLINE=84245824; PubMed=6330561;
RA Saito H., Kranz D.M., Takagaki Y., Hayday A.C., Eisen H.N.,
RA Tonegawa S.;
RT "Complete primary structure of a heterodimeric T-cell receptor
RT deduced from cDNA sequences."
RL Nature 309:757-762(1984).
CC -!- MISCELLANEOUS: THIS MRNA WAS ISOLATED FROM A CYTOTOXIC
CC T-LYMPHOCYTE. THE GENE CORRESPONDING TO THIS MRNA IS REARRANGED
CC SPECIFICALLY IN T CELLS AND ITS ORGANIZATION IS SIMILAR TO AN IG
CC GENE, WITH V (OR V+D), J, AND C REGIONS.
DR PIR; A02018; RWMSV1.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW T-cell; Receptor; Signal.
FT SIGNAL 1 18
FT CHAIN 19 135 T-CELL RECEPTOR GAMMA CHAIN V REGION
FT V108A.
FT DOMAIN 19 116 V SEGMENT.
FT DOMAIN 117 135 J SEGMENT.
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 15930 MW; 402145C95E924D7D CRC64;

Query Match 59.6%; Score 34; DB 1; Length 135;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | |
Db 3 LLRWFTSCCL 12

Search completed: July 16, 2002, 08:00:43
Job time: 821 sec
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:45:57 ; Search time 89.54 Seconds
(without alignments)
19.320 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL_19:*
- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	57	100.0	180	4	Q9Y479	Q9y479 homo sapien
2	44	77.2	151	4	Q9UJK3	Q9ujk3 homo sapien
3	44	77.2	593	4	Q96NH3	Q96nh3 homo sapien
4	38	66.7	65	1	Q46517	Q46517 desulfuroco
5	38	66.7	152	12	Q9PX35	Q9px35 equine arte
6	38	66.7	152	12	Q9PX34	Q9px34 equine arte
7	38	66.7	152	12	Q9QKH1	Q9qkh1 equine arte
8	38	66.7	152	12	Q9QKG6	Q9qkg6 equine arte
9	38	66.7	152	12	Q9QKF2	Q9qkf2 equine arte
10	38	66.7	273	5	Q962M9	Q962m9 plasmodium
11	38	66.7	408	16	Q9KRM7	Q9krm7 vibrio chol
12	38	66.7	423	5	O02168	O02168 caenorhabdi
13	38	66.7	996	10	Q9SGP2	Q9sgp2 arabidopsis
14	37.5	65.8	83	12	Q9WGD6	Q9wgd6 human papil
15	37	64.9	317	5	O97336	O97336 plasmodium
16	37	64.9	783	3	O14411	O14411 candida alb

17	37	64.9	1189	5	Q9VQ78	Q9vq78 drosophila
18	36	63.2	70	12	O90748	O90748 encephalomy
19	36	63.2	71	12	O90751	O90751 encephalomy
20	36	63.2	218	10	Q9LRK4	Q9lrk4 arabidopsis
21	36	63.2	223	10	Q9LRK5	Q9lrk5 arabidopsis
22	36	63.2	255	11	Q9JL02	Q9jl02 rattus norv
23	36	63.2	257	10	Q9LRK3	Q9lrk3 arabidopsis
24	36	63.2	258	10	Q9LRK2	Q9lrk2 arabidopsis
25	36	63.2	288	17	Q97WU4	Q97wu4 sulfolobus
26	36	63.2	298	4	Q9HD97	Q9hd97 homo sapien
27	36	63.2	299	4	Q9UBK4	Q9ubk4 homo sapien
28	36	63.2	299	4	Q9UGN4	Q9ugn4 homo sapien
29	36	63.2	301	4	O95100	O95100 homo sapien
30	36	63.2	311	10	Q9LJW1	Q9ljw1 arabidopsis
31	36	63.2	335	5	Q9XYA7	Q9xya7 drosophila
32	36	63.2	351	10	Q9FE04	Q9fe04 arabidopsis
33	36	63.2	376	4	Q969X9	Q969x9 homo sapien
34	36	63.2	379	4	Q96P06	Q96p06 homo sapien
35	36	63.2	383	4	Q13880	Q13880 homo sapien
36	36	63.2	415	4	Q9NXR7	Q9nxr7 homo sapien
37	35.5	62.3	70	12	Q9WA26	Q9wa26 human papil
38	35.5	62.3	70	12	Q9W9S8	Q9w9s8 human papil
39	35.5	62.3	70	12	Q9W9F2	Q9w9f2 human papil
40	35.5	62.3	70	12	Q9W8H7	Q9w8h7 human papil
41	35.5	62.3	70	12	Q9WIV2	Q9wiv2 human papil
42	35.5	62.3	70	12	Q9WIV3	Q9wiv3 human papil
43	35.5	62.3	70	12	Q9WIV4	Q9wiv4 human papil
44	35.5	62.3	70	12	Q9WIV6	Q9wiv6 human papil
45	35.5	62.3	70	12	Q9WIV7	Q9wiv7 human papil

ALIGNMENTS

RESULT 1

Q9Y479 ID Q9Y479 PRELIMINARY; PRT; 180 AA.
AC Q9Y479;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE LAGE-1S PROTEIN (CANCER/TESTIS ANTIGEN 2).
GN LAGE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MELANOMA;
RX MEDLINE=99325550; PubMed=103999963;
RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT unexpected translation product of LAGE-1.";
RL Int. J. Cancer 82:442-448(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
RA Patlan H., Ciccodicola A., Kenwrick S., Platzner M., D'Urso M.,
RA Nelson D.L.;
RT "Multiple pathogenic and benign genomic rearrangements occur at a 35-
RT kb duplication involving the NEMO and the LAGE2 genes.";
RL Hum. Mol. Genet. 0:0-0(2001).
DR EMBL; AJ012834; CAA10194.1; -.
DR EMBL; AF277315; AAL27015.1; -.
SQ SEQUENCE 180 AA; 18236 MW; 9077FAF953543A25 CRC64;

Query Match 100.0%; Score 57; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10

Db	158	LLMWITQCFL 167		
RESULT	2			
Q9UJK3		PRELIMINARY;	PRT;	151 AA.
ID	Q9UJK3			
AC	Q9UJK3			
DT	01-MAY-2000	(TReMBLrel. 13, Created)		
DT	01-MAY-2000	(TReMBLrel. 13, Last sequence update)		
DT	01-DEC-2001	(TReMBLrel. 19, Last annotation update)		
DE	DJ310J6.1	(NOVEL PROTEIN) (FRAGMENT).		
GN	DJ310J6.1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Blakey S.;			
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AL035593; CAB56526.1; -.			
FT	NON_TER 1			
SQ	SEQUENCE 151 AA; 17990 MW; 9895001E4CF4B6DE CRC64;			
Query Match		77.2%;	Score 44;	DB 4; Length 151;
Best Local Similarity		87.5%;	Pred. No. 1.5;	
Matches	7; Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
QY	2	LMWITQCF 9		
Db	52	LQWITQCF 59		
RESULT	3			
Q96NH3		PRELIMINARY;	PRT;	593 AA.
ID	Q96NH3			
AC	Q96NH3;			
DT	01-DEC-2001	(TReMBLrel. 19, Created)		
DT	01-DEC-2001	(TReMBLrel. 19, Last sequence update)		
DT	01-DEC-2001	(TReMBLrel. 19, Last annotation update)		
DE	CDNA FLJ30899 FIS, CLONE FEBRA2005726.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BRAIN;			
RA	Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,			
RA	Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,			
RA	Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,			
RA	Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,			
RA	Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,			
RA	Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,			
RA	Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;			
RT	"NEDO human cDNA sequencing project.";			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK055461; BAB70925.1; -.			
SQ	SEQUENCE 593 AA; 68636 MW; B3295013BB2225BC CRC64;			
Query Match		77.2%;	Score 44;	DB 4; Length 593;
Best Local Similarity		87.5%;	Pred. No. 5.1;	
Matches	7; Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
QY	2	LMWITQCF 9		
Db	494	LQWITQCF 501		
RESULT	4			

Q46517		PRELIMINARY;	PRT;	65 AA.
ID	Q46517			
AC	Q46517;			
DT	01-NOV-1996	(TReMBLrel. 01, Created)		
DT	01-NOV-1996	(TReMBLrel. 01, Last sequence update)		
DT	01-DEC-2001	(TReMBLrel. 19, Last annotation update)		
DE	ORFD 65	(FRAGMENT).		
OS	Desulfurococcus mobilis.			
OC	Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;			
OC	Desulfurococcus.			
OX	NCBI_TaxID=2274;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=DSM 2126;			
RX	MEDLINE=95206243; PubMed=7898436;			
RA	Ceccarelli E., Bocchetta M., Creti R., Sanangelantoni A.M., Tiboni O.,			
RA	Cammarano P.;			
RT	"Chromosomal organization and nucleotide sequence of the genes for			
RT	elongation factors EF-lalpha and EF-2 and ribosomal proteins S7 and			
RT	S10 of the hyperthermophilic archaeum Desulfurococcus mobilis.";			
RL	Mol. Gen. Genet. 246:687-696(1995).			
DR	EMBL; X73582; CAA51989.1; -.			
FT	NON_TER 65			
SQ	SEQUENCE 65 AA; 7597 MW; B51DEF4F5C84E0F8 CRC64;			
Query Match		66.7%;	Score 38;	DB 1; Length 65;
Best Local Similarity		60.0%;	Pred. No. 7.8;	
Matches	6; Conservative	1;	Mismatches	3; Indels 0; Gaps 0;
QY	1	LLMWITQCFL 10		
Db	6	LTMWYARCF 15		
RESULT	5			
Q9PX35		PRELIMINARY;	PRT;	152 AA.
ID	Q9PX35			
AC	Q9PX35;			
DT	01-MAY-2000	(TReMBLrel. 13, Created)		
DT	01-MAY-2000	(TReMBLrel. 13, Last sequence update)		
DT	01-DEC-2001	(TReMBLrel. 19, Last annotation update)		
DE	ORF4.			
OS	Equine arteritis virus (EAV).			
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;			
OC	Arteriviridae; Arterivirus.			
OX	NCBI_TaxID=11047;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BT-PA96, R1, AND P1;			
RX	MEDLINE=99394666; PubMed=10466790;			
RA	Balasuriya U.B.R., Hedges J.F., Nadler S.A., McCollum W.H.,			
RA	Timoney P.J., MacLachlan N.J.;			
RT	"Genetic Stability of Equine Arteritis Virus during Horizontal and			
RT	Vertical Transmission in an Outbreak of Equine Viral Arteritis.";			
RL	J. Gen. Virol. 80:1949-1958(1999).			
DR	EMBL; AF118781; AAD54755.1; -.			
DR	EMBL; AF118773; AAD54707.1; -.			
DR	EMBL; AF118775; AAD54719.1; -.			
DR	InterPro; IPR004257; GP4.			
DR	Pfam; PF03010; GP4; 1.			
SQ	SEQUENCE 152 AA; 17150 MW; 5E47F3CD85E193B4 CRC64;			
Query Match		66.7%;	Score 38;	DB 12; Length 152;
Best Local Similarity		50.0%;	Pred. No. 17;	
Matches	5; Conservative	3;	Mismatches	2; Indels 0; Gaps 0;
QY	1	LLMWITQCFL 10		
Db	143	LVRWVQQCYL 152		

RESULT 6									
Q9PX34 Q9PX34 PRELIMINARY; PRT; 152 AA.									
AC	Q9PX34; Q9PX34; PRELIMINARY; PRT; 152 AA.								
DT	01-MAY-2000 (TrEMBLrel. 13, Created)								
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)								
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)								
DE	ORF4.								
OS	Equine arteritis virus (EAV).								
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;								
OC	Arteriviridae; Arterivirus.								
OX	NCBI_TaxID=11047;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=P2, A2, A3, AND A4;								
RX	MEDLINE=99394666; PubMed=10466790;								
RA	Balasuriya U.B.R.; Hedges J.F., Nadler S.A., McCollum W.H.,								
RA	Timoney P.J., MacLachlan N.J.;								
RT	"Genetic Stability of Equine Arteritis Virus during Horizontal and								
RT	Vertical Transmission in an Outbreak of Equine Viral Arteritis.";								
RL	J. Gen. Virol. 80:1949-1958(1999).								
DR	EMBL; AF118776; AAD54725.1; -.								
DR	EMBL; AF118770; AAD54689.1; -.								
DR	EMBL; AF118771; AAD54695.1; -.								
DR	EMBL; AF118772; AAD54701.1; -.								
DR	InterPro; IPR004257; GP4.								
DR	Pfam; PF03010; GP4; 1.								
SQ	SEQUENCE 152 AA; 17124 MW; 5F8FF3D15420985F CRC64;								
Query Match 66.7%; Score 38; DB 12; Length 152;									
Best Local Similarity 50.0%; Pred. No. 17;									
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;									
QY	1 LLMWITQCFL 10								
	: : :								
Db	143 LVRWVQQCYL 152								
RESULT 7									
Q9QKH1 Q9QKH1 PRELIMINARY; PRT; 152 AA.									
ID	Q9QKH1 Q9QKH1 PRELIMINARY; PRT; 152 AA.								
AC	Q9QKH1; Q9QKH1; PRELIMINARY; PRT; 152 AA.								
DT	01-MAY-2000 (TrEMBLrel. 13, Created)								
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)								
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)								
DE	ORF4.								
OS	Equine arteritis virus (EAV).								
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;								
OC	Arteriviridae; Arterivirus.								
OX	NCBI_TaxID=11047;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=A1;								
RX	MEDLINE=99394666; PubMed=10466790;								
RA	Balasuriya U.B., Hedges J.F., Nadler S.A., McCollum W.H.,								
RA	Timoney P.J., MacLachlan N.J.;								
RT	"Genetic stability of equine arteritis virus during horizontal and								
RT	vertical transmission in an outbreak of equine viral arteritis.";								
RL	J. Gen. Virol. 80:1949-1958(1999).								
DR	EMBL; AF118769; AAD54683.1; -.								
DR	InterPro; IPR004257; GP4.								
DR	Pfam; PF03010; GP4; 1.								
SQ	SEQUENCE 152 AA; 16995 MW; 5F8FE7815B70835F CRC64;								
Query Match 66.7%; Score 38; DB 12; Length 152;									
Best Local Similarity 50.0%; Pred. No. 17;									
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;									
QY	1 LLMWITQCFL 10								
	: : :								
Db	143 LVRWVQQCYL 152								

```
RESULT 10
Q962M9          PRELIMINARY;          PRT;    273 AA.
AC  Q962M9;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  PVIH14025_P.
GN  PVIH14025C.
OS  Plasmodium vivax.
OC  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX  NCBI_TaxID=5855;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Tchavtchitch M., Fischer K., Huestis R., Saul A.;
RT  "The sequence of 200 kb portion of a Plasmodium vivax chromosome
RT  reveals a high degree of conservation with P. falciparum chromosome
RT  3.";
RL  Mol. Biochem. Parasitol. 0:0-0(2001).
DR  EMBL; AY003872; AAF99451.1; -.
SQ  SEQUENCE 273 AA; 32028 MW; 73F0E1666635A30C CRC64;

Query Match          66.7%; Score 38; DB 5; Length 273;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  1 LLMWITQCF 9
    ||:| |||
Db  27 LLWTQCF 35

RESULT 11
Q9KRM7          PRELIMINARY;          PRT;    408 AA.
AC  Q9KRM7;
DT  01-OCT-2000 (TrEMBLrel. 15, Created)
DT  01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  HYPOTHETICAL PROTEIN VC1609.
GN  VC1609.
OS  Vibrio cholerae.
OC  Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX  NCBI_TaxID=666;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=EL TOR N16961 / SEROTYPE O1;
RX  MEDLINE=20406833; PubMed=10952301;
RA  Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA  Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA  Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA  Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA  McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA  Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA  Fraser C.M.;
RT  "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT  cholerae.";
RL  Nature 406:477-483(2000).
DR  EMBL; AE004238; AAF94763.1; -.
DR  TIGR; VC1609; -.
KW  Complete proteome.
SQ  SEQUENCE 408 AA; 44619 MW; B786CB2501E37C8C CRC64;

Query Match          66.7%; Score 38; DB 16; Length 408;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  2 LMWITQCF 9
    |:|: |||
Db  345 LVWLAQCF 352

Query Match          66.7%; Score 38; DB 16; Length 408;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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RESULT 12
O02168          PRELIMINARY;          PRT;    423 AA.
AC  O02168;
DT  01-JUL-1997 (TrEMBLrel. 04, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  HYPOTHETICAL 47.5 KDA PROTEIN.
GN  T20F7.6.
OS  Caenorhabditis elegans.
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC  Rhabditidae; Peloderinae; Caenorhabditis.
OX  NCBI_TaxID=6239;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BRISTOL N2;
RX  MEDLINE=99069613; PubMed=9851916;
RA  None;
RT  "Genome sequence of the nematode C. elegans: a platform for
RT  investigating biology. The C. elegans Sequencing Consortium.";
RL  Science 282:2012-2018(1998).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BRISTOL N2;
RA  Miller N., Gattung S.;
RT  "The sequence of C. elegans cosmid T20F7.";
RL  Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BRISTOL N2;
RA  Waterston R.;
RT  "Direct Submission.";
RL  Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; U97550; AAK18981.2; -.
KW  Hypothetical protein.
SQ  SEQUENCE 423 AA; 47451 MW; 6997065D515E7B21 CRC64;

Query Match          66.7%; Score 38; DB 5; Length 423;
Best Local Similarity 62.5%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  2 LMWITQCF 9
    |:||| ||:
Db  43 LLWINQCY 50

RESULT 13
Q9SGP2          PRELIMINARY;          PRT;    996 AA.
AC  Q9SGP2;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  F3M18.12.
OS  Arabidopsis thaliana (Mouse-ear cress).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX  NCBI_TaxID=3702;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA  Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA  Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA  Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsy N., Nguyen M.,
RA  Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA  Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA  Ecker J.R.;
RT  "Genomic sequence for Arabidopsis thaliana BAC F3M18 from chromosome
RT  I.";
RL  Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
```

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; AC010155; AAF16764.1; -.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00560; LRR; 22.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00370; LRR; 18.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 996 AA; 108929 MW; 9C9A6A708A1F933A CRC64;

Query Match 66.7%; Score 38; DB 10; Length 996;
Best Local Similarity 55.6%; Pred. No. 97;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LMWITQCFL 10
:||:|:| |
Db 209 VMWLTECHL 217

RESULT 14
Q9WGD6 PRELIMINARY; PRT; 83 AA.
ID Q9WGD6;
AC Q9WGD6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E5 PROTEIN.
GN E5.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IS808;
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-IS808;
RX MEDLINE=99190418; PubMed=10091997;
RA Eriksson A., Herron J.R., Yamada T., Wheeler C.M.;
RT "Human papillomavirus type 16 variant lineages characterized by
nucleotide sequence analysis of the E5 coding segment and the E2 hinge
region.";
RL J. Gen. Virol. 80:595-600(1999).
DR EMBL; AF120707; AAD24035.1; -.
DR InterPro; IPR004270; Papilloma_E5.
DR Pfam; PF03025; Papilloma_E5; 1.
SQ SEQUENCE 83 AA; 9387 MW; B57D5DD3DD77CB7E CRC64;

Query Match 65.8%; Score 37.5; DB 12; Length 83;
Best Local Similarity 53.3%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 0; Indels 5; Gaps 1;

Qy 1 LLMWIT-----QCFL 10
||:|:| |
Db 47 LLLWITAASAFRCFL 61

RESULT 15
O97336 PRELIMINARY; PRT; 317 AA.
ID O97336;
AC O97336;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PFC0085C, MAL3P8.15 PROTEIN.
GN PFC0085C, MAL3P8.15.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-3D7;
RX MEDLINE=99376085; PubMed=10448855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
falciparum .";
RL Nature 400:532-538(1999).
DR EMBL; AL034560; CAB39133.2; -.
SQ SEQUENCE 317 AA; 37389 MW; 26CF0DC38C651474 CRC64;

Query Match 64.9%; Score 37; DB 5; Length 317;
Best Local Similarity 55.6%; Pred. No. 51;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9
: ||:|:| |
Db 51 IFIWICQCF 59

Search completed: July 16, 2002, 07:59:50
Job time: 833 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run On: July 16, 2002, 07:39:52 ; Search time 113.12 Seconds
(without alignments)
9.819 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
6: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
7: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	20	AA1980
2	57	100.0	10	21	AA1981
3	57	100.0	11	19	AA1982
4	57	100.0	11	20	AA1983
5	57	100.0	11	21	AA1984
6	57	100.0	11	21	AA1985
7	57	100.0	11	21	AA1986
8	57	100.0	11	21	AA1987
9	57	100.0	11	21	AA1988
10	57	100.0	11	22	AA1989
11	57	100.0	11	22	AA1990

12	57	100.0	11	22	AA1991
13	57	100.0	11	22	AA1992
14	57	100.0	11	22	AA1993
15	57	100.0	11	22	AA1994
16	57	100.0	11	22	AA1995
17	57	100.0	11	22	AA1996
18	57	100.0	11	22	AA1997
19	57	100.0	11	22	AA1998
20	57	100.0	14	22	AA1999
21	57	100.0	14	22	AA2000
22	57	100.0	14	22	AA2001
23	57	100.0	14	22	AA2002
24	57	100.0	14	22	AA2003
25	57	100.0	14	22	AA2004
26	57	100.0	20	22	AA2005
27	57	100.0	27	22	AA2006
28	57	100.0	180	19	AA2007
29	57	100.0	180	19	AA2008
30	57	100.0	180	19	AA2009
31	57	100.0	180	20	AA2010
32	57	100.0	180	21	AA2011
33	57	100.0	180	21	AA2012
34	57	100.0	180	21	AA2013
35	57	100.0	180	21	AA2014
36	57	100.0	180	22	AA2015
37	57	100.0	180	22	AA2016
38	57	100.0	180	22	AA2017
39	57	100.0	180	22	AA2018
40	57	100.0	397	22	AA2019
41	53	93.0	9	20	AA2020
42	53	93.0	9	20	AA2021
43	53	93.0	9	21	AA2022
44	53	93.0	9	22	AA2023
45	53	93.0	9	22	AA2024

Human NY-ESO-1 ant
HLA-A2 binding NY-
NY-ESO-1 human leu
Cytolytic T cell 1
HLA-A2 binding pep
Human NY-ESO-1 CTL
Exemplary antigen
Human NY ESO-1 pro
Human HLA-DP restr
Human HLA-DP restr
Human HLA-DP restr
Human HLA-DP restr
Human modified NY
Human modified NY
Human ESO p156-175
Human HLA-DP restr
Human LAGE-1 clone
Human NY-ESO-1 pro
Cancer associated
Human cancer antig
Human oesophageal
Human LAGE-1 splic
Human tumour antig
Human tumour antig
Amino acid sequenc
Human NY ESO-1 pro
Human NY-ESO-1 tum
Human NY-ESO-1 pro
NY-ESO-IC-HER-2 me
Human cancer antig
Human cancer antig
NY-ESO-1 derived p
Cancer testis tumo
Cancer testis tumo

ALIGNMENTS

RESULT 1
AA1980
ID AA1980 standard; Peptide; 10 AA.
XX
AC AA1980;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO1980206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.
XX

PT Cancer antigen NY ESO1/CAG-3
XX
PS Example 10; Page 42; 88pp; English.
XX
CC This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC The present peptide (ranked 16) corresponds to amino acid residues
CC 158-167 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 57; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 1 llmwitqcfl 10

RESULT 2
AAAY52434
ID AAY52434 standard; peptide; 10 AA.
XX
AC AAY52434;
XX
DT 15-FEB-2000 (first entry)
XX
DE Human tumour antigen NY-ESO-1 peptide #7.
XX
KW Cancer; tumour; antigen; MHC; major histocompatibility complex; Class I;
KW T-cell; cytotoxic; stimulation; proliferation; treatment;
KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW lymphoma.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9953938-A1.
XX
PD 28-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US06875.
XX
PR 17-APR-1998; 98US-0062422.
PR 02-OCT-1998; 98US-0165546.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX
DR WPI; 2000-038483/03.
XX
PT Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes .
XX
PS Claim 55; Page 20; 49pp; English.
XX

CC Peptides #4-#7 (AAY52431-Y52434) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (AAY52430) which contain the motif LLMWIT
CC (AAY52441). These sequences can bind to MHC (major histocompatibility
CC Class I HLA-A2 molecules, thereby stimulating proliferation of
CC cytotoxic T-cells. cDNA encoding NY-ESO-1 was initially isolated
CC from an oesophagus squamous cell cancer cDNA library. Tissue
CC localisation studies revealed it to be expressed at high levels
CC in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC These NY-ESO-1-derived peptides may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of
CC cancers (such as melanoma, breast cancer, prostate cancer, lung
CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 57; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 1 llmwitqcfl 10

RESULT 3
AAW62585
ID AAW62585 standard; peptide; 11 AA.
XX
AC AAW62585;
XX
DT 17-SEP-1998 (first entry)
XX
DE Cancer associated antigen peptide.
XX
KW Cancer associated antigen; NY-ESO-1; regression; progression; onset;
KW cancer; treatment; diagnosis.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9814464-A1.
XX
PD 09-APR-1998.
XX
PF 15-SEP-1997; 97WO-US16335.
XX
PR 03-OCT-1996; 96US-0725182.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Chen Y, Drijfhout JW, Gure A, Jager E, Knuth A;
PI Old LJ, Scanlan M;
XX
DR WPI; 1998-286417/25.
XX
PT New isolated cancer associated antigen - is used to develop products
PT for the diagnosis and treatment of cancers and for monitoring cancer
PT therapy
XX
PS Claim 33; Page 17; 49pp; English.
XX
CC Peptides AAW62585-87 are derived from cancer associated antigen
CC NY-ESO-1, and are stimulators of cytotoxic T-cells. The specification
CC describes a method for determining regression, progression of onset of a
CC cancerous condition, comprising monitoring a sample from a patient
CC with the cancerous condition for a parameter selected from NY-ESO-1
CC protein, a peptide derived from NY-ESO-1 protein and cytolytic

.

CC T cells specific for the peptide and an MHC molecule with which it
CC non-covalently complexes. Methods for the treatment of a cancerous
CC condition are also described. The NY-ESO-1 protein and peptides derived
CC from it can be used for diagnosis and treatment of cancers and to
CC monitor the efficacy of a therapeutic regime.

SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 19; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | |
Db 2 llmwitqcfl 11

RESULT 4
AAV01761
ID AAY01761 standard; Peptide; 11 AA.
XX
AC AAY01761;
XX
DT 25-JUN-1999 (first entry)
XX
DE Exemplary antigenic peptide derived from NY-ESO-1.

XX MAGE-3; tumour associated gene; human leucocyte antigen Class II;
KW autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;
KW osteosarcoma; leukemia; carcinoma.
XX

OS Homo sapiens.
XX
PN WO9914326-A1.
XX
PD 25-MAR-1999.
XX
PF 04-SEP-1998; 98WO-US18601.
XX
PR 12-SEP-1997; 97US-0928615.

XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYVR-) UNIV VRIJE BRUSSEL.
XX
PI Boon-Falleur T, Chaux P, Corthals J, Heirman C;
PI Luiten R, Stroobant V, Thielemans K, Van Der Bruggen P;
XX
DR WPI; 1999-244031/20.

XX Isolated peptides that bind to human leucocyte antigen class II
PT molecules
XX
PS Disclosure; Page 29; 88pp; English.

XX The present sequence represents an exemplary tumour associated peptide
CC antigen. The specification describes a MAGE-3 tumour associated gene.
CC Peptides (AAV01721-25) that bind human leucocyte antigen (HLA) Class II
CC molecules can be derived from the MAGE-3 protein. These peptides and
CC autologous CD4+ cells that bind to a complex of MAGE-3 peptide
CC and HLA Class II, are used to treat MAGE-3 related diseases,
CC particularly cancers (e.g. melanoma, osteosarcoma, leukemia and
CC various forms of carcinoma). The peptides are also used to produce
CC specific antibodies. Detection of of the peptides, e.g. in binding
CC assays, particularly with antibodies, is used for diagnosis of such
CC diseases.

XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | |
Db 2 llmwitqcfl 11

RESULT 5
AAB08702
ID AAB08702 standard; Peptide; 11 AA.
XX
AC AAB08702;
XX
DT 02-JAN-2001 (first entry)
XX
DE Antigenic peptide from tumour rejection antigen NY-ESO-1.

XX Epha3; HLA class II-binding peptide; human leukocyte antigen; antigen;
KW CD4+ T lymphocyte; tumour associated gene; vaccine.

XX Homo sapiens.
OS
XX WO200050589-A1.
PN
XX
PD 31-AUG-2000.
XX
PF 18-FEB-2000; 2000WO-US04326.

XX 22-FEB-1999; 99US-0121170.
PR 08-OCT-1999; 99US-0158566.
XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX
PI Chiari R, Coulie P, Boon-Falleur T;
XX
DR WPI; 2000-572089/53.

XX Novel tyrosine kinase receptor, Epha3 human leukocyte antigen (HLA)
PT class II binding peptide and nucleic acid encoding the receptor, useful
PT for diagnosing and treating conditions characterized by expression of
PT Epha3 gene -
XX

PS Disclosure; Page 35; 107pp; English.

XX AAB08668-B08704 represent antigenic peptides characteristic of tumours.
CC The peptides may be combined in vaccines with a human Epha3 HLA (human
CC leukocyte antigen) class II-binding peptide. Epha3 antigens, when
CC presented by an antigen presenting cell having a HLA class II molecule,
CC effectively induce activation and proliferation of CD4+ T lymphocytes.
CC Epha3 is a tumour associated gene. Epha3 HLA binding peptides are used
CC for selectively enriching a population of T lymphocytes. The peptides
CC are also used for diagnosing a disorder characterized by Epha3 or Epha3
CC HLA binding peptide expression. The peptides are also used to treat a
CC disorder characterized by Epha3 expression. The Epha3 binding peptides
CC are useful in producing vaccines and antibody.

XX Sequence 11 AA;

Query Match 100.0%; Score 57; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | |
Db 2 llmwitqcfl 11

RESULT 6
AAB22790
ID AAB22790 standard; peptide; 11 AA.
XX
AC AAB22790;
XX

DT 22-DEC-2000 (first entry)
XX
DE NY-ESO-1 peptide epitope, SEQ ID NO:1.
XX
KW NY-ESO-1; epitope; CTL response; cytotoxic T lymphocyte; vaccine;
KW immunogenic; adjuvant coadministration; microbial infection;
KW tuberculosis; HIV; hepatitis B virus; hepatitis C virus; cancer.
XX
OS Unidentified.
XX
PN WO200048630-A1.
XX
PD 24-AUG-2000.
XX
PF 17-FEB-2000; 2000WO-AU00110.
XX
PR 17-FEB-1999; 99AU-0008735.
PR 27-JUL-1999; 99AU-0001861.
XX
PA (CSLC-) CSL LTD.
XX
PI Cox JC, Drane DP;
XX
DR WPI; 2000-571930/53.
XX
PT Immunogenic complexes comprising negatively charged organic carrier
PT adjuvants and positively charged antigens for use as vaccines against
PT microbial infection and cancer
XX
PS Example 4; Fig 5a; 111pp; English.
XX
CC The invention relates to a novel immunogenic complex comprising a
CC charged organic carrier and a charged antigen which are
CC electrostatically associated. The complex induces a cytotoxic T
CC lymphocyte (CTL) response. The complex and/or vaccine can be used to
CC treat a disease in a mammal, where the complex/vaccine elicits, induces
CC or otherwise facilitates an immune response which inhibits, halts, delays
CC or prevents the onset or progression of the disease condition. In
CC particular, the disease is a condition resulting from a microbial
CC infection or cancer. Microbial infections which may be treated using the
CC immunogenic complex include human immunodeficiency virus (HIV), hepatitis
CC B, hepatitis C, tuberculosis or a parasitic condition, and cancers which
CC may be treated include melanoma, prostate cancer or breast cancer. The
CC complexes and vaccines simultaneously co-deliver antigen and adjuvant to
CC the same antigen presenting cell, which is often essential for induction
CC of appropriate immune responses. Sequences AAB22790-B22791 represent
CC peptide epitopes of the positively charged protein NY-ESO-1 used in an
CC exemplification of the invention.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db | | | | | | | | | |
2 llmwitqcfl 11

RESULT 7
AAB02630
ID AAB02630 standard; Peptide; 11 AA.
XX
AC AAB02630;
XX
DT 18-AUG-2000 (first entry)
XX
DE Tumour associated peptide antigen from NY-ESO-1 #1.
XX
KW MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;
KW cancer; human; tumour; tumour associated gene product.

XX Homo sapiens.
OS
XX WO200020581-A1.
PN
XX
PD 13-APR-2000.
XX
PF 15-SEP-1999; 99WO-US21230.
XX
PR 05-OCT-1998; 98US-0166448.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYVR-) UNIV VRIJE BRUSSEL.
XX
PI Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P;
PI Schultz ES, Van Snick J, Lethe B, Thielemans K, Corthals J;
PI Heirman C;
XX
DR WPI; 2000-317713/27.
XX
PT New MAGE-A3 class II binding peptides, useful to diagnose and treat
PT tumours, are fragments of MAGE-A3 which bind to and are presented to T
PT lymphocytes by human leukocyte antigen class II molecules
XX
PS Disclosure; Page 33; 119pp; English.
XX
CC The present invention relates to MAGE-A3 (tumour associated gene
CC product) human leukocyte antigen (HLA) class II-binding peptides (see
CC AAB02566-B02595, and AAB02633-B02637). These peptides are presented to T
CC cells in the context of HLA class II molecules. The peptides stimulate
CC the activity and proliferation of CD4+ T lymphocytes. The invention also
CC includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928
CC and AAA37938-A37940). The peptides and nucleotide sequences can be used
CC to create antibodies against the MAGE-A3 peptides, the antibodies,
CC peptides and nucleotide sequences can be used to create a vaccine. The
CC peptides are used to diagnose or treat a disorder characterized by
CC expression of MAGE-3, particularly cancer. The methods can also be used
CC in the diagnosis of disorders associated with MAGE-3 expression. Included
CC in the invention are other human tumour antigens (see AAB02596-B02637),
CC and PCR primers used in the course of the invention (see AAA37929-A37937
CC and AAA37941-A37942).
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db | | | | | | | | | |
2 llmwitqcfl 11

RESULT 8
AAY78469
ID AAY78469 standard; Peptide; 11 AA.
XX
AC AAY78469;
XX
DT 10-MAY-2000 (first entry)
XX
DE NY-ESO-1 derived peptide #1.
XX
KW Cancer; SSX family; SSX-1; SSX-2; SSX-3; SSX-4; SSX-5; NY-ESO-1;
KW HLA binding; human leukocyte antigen; cytolytic T cell; CTL;
KW cytostatic; melanoma; synovial sarcoma.
XX
OS Homo sapiens.
XX
PN WO200000824-A1.
XX
PD 06-JAN-2000.

XX 25-JUN-1999; 99WO-US14493.
PF
XX
PR 26-JUN-1998; 98US-0105839.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Tureci O, Sahin U, Pfreundschuh M, Rammensee G, Stevanovic S;
PI Chen Y, Gure A, Old LJ;
XX
DR WPI; 2000-170933/15.
XX
PT Determining the possible presence of breast, endometrial, colorectal,
PT lung, bladder or head-neck cancer -
XX
PS Example 12; Page 21; 40pp; English.
XX
CC A method has been developed for determining the possible presence of a
CC cancer, which is not melanoma or synovial sarcoma. The method comprises
CC assaying a sample taken from the subject to determine the expression of
CC an SSX gene, and determining the expression as a determination of the
CC possible presence of cancer. Expression of SSX1 gene indicates possible
CC presence of breast, endometrial, colorectal, lung, bladder or head-neck
CC cancer. These cancers are also detected by SSX2 and SSX4 gene
CC expression. SSX2 gene expression additionally indicates possible presence
CC of lymphoma, renal cell cancer, glioma and prostate cancer. Expression
CC of SSX4 gene also indicates possible presence of ovarian or stomach
CC cancer. SSX5 gene expression indicates the same cancers as SSX1, except
CC breast cancer. Determining expression of SSX gene can be used to monitor
CC progress of melanoma or synovial sarcoma, which is not cancer. The
CC SSX-derived peptide complex stimulates proliferation of cytolytic T
CC cells. This is useful for treating cancer, especially melanoma. AAY78464
CC to AAY78468 represent specifically claimed HLA binding peptides for use
CC in the method of the invention. AAZ88452 to AAZ88465 represent PCR
CC primers used in the isolation of SSX genes in the exemplification of the
CC present invention. AAY78469 to AAY78500, and AAY79684 to AAY79762
CC represent peptides derived from SSX proteins or NY-ESO-1, which are used
CC in the exemplification of the present invention.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | | | |
Db 2 llmwitqcfl 11

RESULT 9
AAY52431
ID AAY52431 standard; peptide; 11 AA.
XX
AC AAY52431;
XX
DT 15-FEB-2000 (first entry)
XX
DE Human tumour antigen NY-ESO-1 peptide #4.

XX Cancer; tumour; antigen; MHC; major histocompatibility complex; Class I;
KW T-cell; cytotoxic; stimulation; proliferation; treatment;
KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW lymphoma.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9953938-A1.
XX
PD 28-OCT-1999.

XX 24-MAR-1999; 99WO-US06875.
PF
XX
PR 17-APR-1998; 98US-0062422.
PR 02-OCT-1998; 98US-0165546.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX
DR WPI; 2000-038483/03.
XX
PT Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes -
XX
PS Claim 60; Page 18; 49pp; English.
XX
CC Peptides #4-#7 (AAY52431-Y52434) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (AAY52430) which contain the motif LLMWIT
CC (AAY52441). These sequences can bind to MHC (major histocompatibility
CC Class I HLA-A2 molecules, thereby stimulating proliferation of
CC cytotoxic T-cells. cDNA encoding NY-ESO-1 was initially isolated
CC from an oesophagus squamous cell cancer cDNA library. Tissue
CC localisation studies revealed it to be expressed at high levels
CC in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC These NY-ESO-1-derived peptides may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of
CC cancers (such as melanoma, breast cancer, prostate cancer, lung
CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | | | |
Db 2 llmwitqcfl 11

RESULT 10
AAG67165
ID AAG67165 standard; peptide; 11 AA.
XX
AC AAG67165;
XX
DT 13-NOV-2001 (first entry)
XX

DE Cancer testis tumour antigen NY-ESO-1 derived CTL-stimulating peptide.
KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW HLA; HLA binding peptide; major histocompatibility complex; MHC;
KW tumour; cancer; testis tumour.
XX Homo sapiens.

OS
XX WO200162917-A1.
PN
XX 30-AUG-2001.
PD
XX 22-JAN-2001; 2001WO-US02126.
PF
XX 22-FEB-2000; 2000US-0510635.
PR
XX (LUDW-) LUDWIG INST CANCER RES.
PA

XX PI Lethe B, Boon-Falleur T;
XX DR WPI; 2001-550091/61.
XX PT Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful
XX PT for diagnosing testicular tumours -
XX PS Example 12; Page 24; 50pp; English.
XX CC The present sequence represents a peptide which is derived from cancer
CC CC testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptide
CC CC stimulates cytolytic T cell lines (CTLs). NY-ESO-1 is a molecule that
CC CC is processed to at least one human leukocyte antigen (HLA) binding
CC CC peptide, which binds to Class I and Class II major histocompatibility
CC CC complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis,
CC CC but not normal colon, kidney, liver or brain tissue. The presence or
CC CC level of expression of NY-ESO-1 may be assayed for the diagnosis of
CC CC cancer, especially testis tumours.
XX SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 2 llmwitqcfl 11

RESULT 11
AAE07777
ID AAE07777 standard; peptide; 11 AA.
XX AC AAE07777;
XX DT 06-NOV-2001 (first entry)
XX DE Human wildtype NY ESO-1 peptide, ESOp157-167.
XX KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leukocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX OS Homo sapiens.
XX PN WO200155393-A2.
XX PD 02-AUG-2001.
XX PF 26-JAN-2001; 2001WO-US02765.
XX PR 28-JAN-2000; 2000US-0179004.
XX PR 29-SEP-2000; 2000US-0237107.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Wang R, Rosenberg SA, Zeng G;
XX DR WPI; 2001-496851/54.
XX CC New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX PS Example 14; Page 62; 134pp; English.
XX CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II

CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC wildtype NY ESO-1 peptide, ESOp157-167.
XX SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 2 llmwitqcfl 11

RESULT 12
AAE06849
ID AAE06849 standard; peptide; 11 AA.
XX AC AAE06849;
XX DT 16-OCT-2001 (first entry)
XX DE Human NY-ESO-1 antigenic peptide #1.
XX KW MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44;
KW tumour cell; immunostimulant; antigen presentation; cancer; melanoma;
KW CD8+ cytotoxic T lymphocyte; colorectal; prostate; gastric carcinoma;
KW myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cytostatic;
KW gene therapy; tumour rejection antigen; TRA; human; NY-ESO-1;
KW MHC; major histocompatibility complex.
XX OS Homo sapiens.
XX PN WO200153833-A1.
XX PD 26-JUL-2001.
XX PF 19-JAN-2001; 2001WO-US02008.
XX PR 20-JAN-2000; 2000US-0177242.
XX PR 25-OCT-2000; 2000US-0243212.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Luiten R, Boon-Falleur T, Van Der Bruggen P, Stroobant V;
PI Demotte N, Schultz E;
XX DR WPI; 2001-488724/53.
XX CC Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or
PT HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, used
PT in diagnosis and treatment of a disorder characterized by expression of
PT MAGE-A1 or -A3 -
XX PS Disclosure; Page 28; 103pp; English.
XX CC The invention relates to functional variants and isolated mimetics of a
CC MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide,
CC or of a MAGE-A3 HLA-B35 binding peptide, identified by methods described

CC in the specification. MAGE genes encode tumour rejection antigens
CC (TRAS) presented to T lymphocytes by HLA-B35 and HLA-B44 molecules.
CC The MAGE antigenic peptide acts by binding to HLA molecules
CC on tumour cells and stimulating recognition of these cells and thus
CC signalling them to the immune system for destruction. The peptide when
CC presented by HLA molecule induces the activation and stimulation of
CC CD8+ cytotoxic T lymphocytes. The MAGE antigenic peptide is used to
CC treat and diagnose disorders characterised by expression of MAGE-A1
CC or -A3. Disorders include cancers e.g melanomas, oesophageal, lung,
CC head and neck, breast, colorectal, prostate, renal, bladder,
CC hepatocellular, papillary thyroid and gastric carcinomas, myelomas,
CC brain tumours, sarcomas, seminomas, and ovarian tumours. The present
CC sequence is human NY-ESO-1 tumour associated antigenic peptide
CC presented by major histocompatibility complex (MHC) HLA-A2. The
CC antigenic peptide is used in combination with peptides of the
CC invention for inducing an immune response.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 2 lllmwtqcfl 11

RESULT 13
AAB85298
ID AAB85298 standard; peptide; 11 AA.
XX
AC AAB85298;
XX
DT 17-SEP-2001 (first entry)
XX
DE HLA-A2 binding NY-ESO-1 peptide #1.
XX
KW NY-ESO-1; human leukocyte antigen; HLA; lysis; cytolytic T cell; CTL;
KW HLA-A2; T-cell sorter; tumor; immune tetramer.
XX Homo sapiens.
OS
XX
PN WO200136453-A2.
XX
PD 25-MAY-2001.
XX
PF 08-NOV-2000; 2000WO-US42010.
XX
PR 15-NOV-1999; 99US-0440621.
PR 25-FEB-2000; 2000US-0514036.
PR 29-SEP-2000; 2000US-0676005.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYOX-) UNIV OXFORD.
XX
PI Valmori D, Cerottini J, Romero P, Cerundolo V;
XX WPI; 2001-451454/48.
DR
XX
PT Novel isolated NY-ESO-1 nonapeptide useful for determining if a cell
PT presents human leukocyte antigen-A2 molecule on its surface, binds to
PT human leukocyte antigen molecules and provokes lysis by cytolytic T
PT cells -
XX
PS Example 1; Page 4; 38pp; English.
XX
CC The invention provides NY-ESO-1 peptide derivatives which bind to human
CC leukocyte antigen (HLA) molecules and provokes lysis by cytolytic T cells
CC (CTLs). The NY-ESO-1 nonapeptide is of formula SLLMWITQX, where X is an
CC amino acid having an uncharged polar side chain. The NY-ESO-1 peptide
CC derivatives are useful for determining if a cell presents an HLA-A2

CC molecule on its surface, by contacting a sample containing the cell with
CC the peptide or its derivative, and determining binding between them,
CC where the binding is indicative of HLA-A2 on the surface of the cell.
CC The NY-ESO-1 peptides and analogues are useful therapeutically, for
CC administration to a patient who is HLA-A2 positive and expresses NY-ESO-1
CC in connection with the pathology, as well as diagnostically, i.e. to
CC determine if HLA-A2 positive cells are present, or if relevant CTLs are
CC present. They are also useful for determining the presence of CTLs in a
CC sample. The peptides are useful as T-cell sorters, when incorporated into
CC immune tetramers. The present sequence represents a NY-ESO-1 peptide that
CC can bind to HLA-A2 molecule.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 2 lllmwtqcfl 11

RESULT 14
AAE02119
ID AAE02119 standard; peptide; 11 AA.
XX
AC AAE02119;
XX
DT 31-JUL-2001 (first entry)
XX
DE NY-ESO-1 human leukocyte antigen-A2-binding peptide #1.
XX
KW Human; cytostatic; immunogen; NY-ESO-1; human leukocyte antigen;
KW HLA; CD8; cytotoxic T lymphocyte; cancer; carcinoma; myeloma;
KW brain tumour; sarcoma; vaccine; gene therapy.
XX Homo sapiens.
OS
XX WO200129220-A2.
PN
XX 26-APR-2001.
PD
XX 19-OCT-2000; 2000WO-US28852.
PF
XX 19-OCT-1999; 99US-0160374.
PR
XX 01-FEB-2000; 2000US-0179570.
PR
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX Heidecker L, Van Den Eynde B, Boon-Falleur T, Brasseur F;
PI WPI; 2001-328498/34.
XX
DR New antigenic peptides derived from MAGE-A12 polypeptides, useful for
XX diagnosis and treatment of cancer, such as bladder, lung, breast,
XX brain, prostate and renal carcinomas -
PS Disclosure; Page 21; 69pp; English.
XX
CC The patent discloses antigenic peptides derived from MAGE-A12
CC protein and presented by human leukocyte antigens (HLAs). These
CC antigenic peptides when presented by an antigen presenting cell
CC having a HLA class I molecule, effectively induce the activation
CC and proliferation of CD8+ cytotoxic T lymphocytes (CTLs). MAGE-A12
CC is useful for treating a subject having a disorder characterised by
CC expression of MAGE-A12. The protein microarray comprising MAGE-A12
CC is useful for diagnosing a disorder, especially cancer, by determining
CC the binding of an antibody, T lymphocytes or a HLA molecule isolated
CC from the subject suspected of having the disorder characterised by the
CC expression of MAGE-A12. MAGE-A12 is useful for treating cancers,
CC including bladder carcinomas, melanomas, oesophageal, lung, head and

CC neck, breast, colorectal carcinomas, myelomas, brain tumours, sarcomas,
CC prostate and renal carcinomas and to produce antibodies. MAGE-A12
CC antibodies are useful for diagnosing disorders characterised by
CC expression of MAGE-A12 immunogenic polypeptide. These MAGE-A12 peptides
CC are used as vaccines. They are also used in gene therapy.
CC The present sequence is an antigenic peptide derived from NY-ESO-1. This
CC peptide which is characteristic of tumours is presented by HLA-A2 MHC
CC (major histocompatibility complex) and is recognised by CTLs.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 2 llmwitqcfl 11

RESULT 15
AAU01536
ID AAU01536 standard; Peptide; 11 AA.

XX AC AAU01536;

XX DT 18-JUL-2001 (first entry)

XX DE Cytolytic T cell line stimulator peptide #1.

XX KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody; cytolytic T cell line.

XX OS Homo sapiens.

XX PN WO200123560-A2.

XX PD 05-APR-2001.

XX PF 26-SEP-2000; 2000WO-US26411.

XX PR 29-SEP-1999; 99US-0408036.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Tureci O, Sahin U, Pfreundschuh M;

XX DR WPI; 2001-266156/27.

XX PT Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid
PT sequence found in tumour rejection antigen precursor used for
PT stimulating proliferation of helper T cells -

PS Example 12; Page 17; 62pp; English.

XX CC The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which efficiently stimulates cytolytic T cell lines.
CC NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to major
CC histocompatibility complex (MHC) Class II molecules such as human
CC leukocyte antigen-determining region (HLA-DR) molecules and stimulate
CC proliferation of helper T cells. The peptides can be administered to an
CC HLA-DR positive subject in order to stimulate the helper T cells. An MHC
CC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell
CC or present in free form is useful for this stimulation. The nucleic acid
CC is useful for screening for a cancerous condition, which involves
CC contacting a subject sample to a cell line transfected with the
CC immunoreactive cell (helper T cell), where interaction is indicative of
CC cancer. In addition, a sample from a patient (for example, a body fluid

CC or tissue) can be monitored for the amount of the complex present in the
CC bloodstream. This is useful for determining regression, progression or
CC onset of a cancerous condition. The method involves contacting the sample
CC with a radioactive labelled or enzyme labelled monoclonal antibody which
CC specifically binds with the complex.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 2 llmwitqcfl 11

Search completed: July 16, 2002, 07:45:50
Job time: 358 sec

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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:43:02 ; Search time 477.3 Seconds
(without alignments)
7.374 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
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1	57	100.0	10 15	US-09-165-546A-7	Sequence 7, Appli
2	57	100.0	10 19	US-09-529-206-92	Sequence 92, Appl
3	57	100.0	10 19	US-09-529-206A-92	Sequence 92, Appl
4	57	100.0	10 19	US-09-529-206B-92	Sequence 92, Appl
5	57	100.0	11 1	PCT-US00-04326-42	Sequence 42, Appl
6	57	100.0	11 1	PCT-US99-06875-4	Sequence 4, Appli
7	57	100.0	11 15	US-09-165-546A-4	Sequence 4, Appli

8	57	100.0	11	17	US-09-336-091-41	Sequence 41, Appl
9	57	100.0	11	17	US-09-396-315-79	Sequence 79, Appl
10	57	100.0	11	18	US-09-408-036B-4	Sequence 4, Appli
11	57	100.0	11	18	US-09-440-621-1	Sequence 1, Appli
12	57	100.0	11	19	US-09-510-635A-4	Sequence 4, Appli
13	57	100.0	11	19	US-09-574-749-33	Sequence 33, Appl
14	57	100.0	11	20	US-09-676-005B-1	Sequence 1, Appli
15	57	100.0	11	20	US-09-692-401-43	Sequence 43, Appl
16	57	100.0	11	20	US-09-697-884-79	Sequence 79, Appl
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18	57	100.0	11	21	US-09-751-798-4	Sequence 4, Appli
19	57	100.0	11	21	US-09-766-889A-50	Sequence 50, Appl
20	57	100.0	11	23	US-09-913-756-42	Sequence 42, Appl
21	57	100.0	11	24	US-10-023-182-4	Sequence 4, Appli
22	57	100.0	122	26	US-60-336-968-17	Sequence 17, Appl
23	57	100.0	180	11	US-08-791-495-7	Sequence 7, Appli
24	57	100.0	180	11	US-08-791-495-9	Sequence 9, Appli
25	57	100.0	180	17	US-09-341-829A-7	Sequence 7, Appli
26	57	100.0	180	17	US-09-341-829A-9	Sequence 9, Appli
27	57	100.0	180	17	US-09-392-714-25	Sequence 25, Appl
28	57	100.0	180	19	US-09-529-206-4	Sequence 4, Appli
29	57	100.0	180	19	US-09-529-206A-3	Sequence 3, Appli
30	57	100.0	180	19	US-09-529-206B-3	Sequence 3, Appli
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35	57	100.0	180	24	US-10-026-066-3	Sequence 3, Appli
36	57	100.0	180	26	US-60-336-968-11	Sequence 11, Appl
37	57	100.0	397	22	US-09-821-883-27	Sequence 27, Appl
38	53	93.0	9	18	US-09-409-455A-123	Sequence 123, App
39	53	93.0	9	19	US-09-529-206-71	Sequence 71, Appl
40	53	93.0	9	19	US-09-529-206-72	Sequence 72, Appl
41	53	93.0	9	19	US-09-529-206A-71	Sequence 71, Appl
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44	53	93.0	9	19	US-09-529-206B-72	Sequence 72, Appl
45	53	93.0	9	22	US-09-833-039-123	Sequence 123, App

ALIGNMENTS

RESULT 1

US-09-165-546A-7
; Sequence 7, Application US/09165546A
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
; MHC CLASS I AND MHC CLASS II MOLECULES, AND
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546A
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998

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; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-165-546A-7

Query Match      100.0%; Score 57; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LLMWITQCFL 10
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Db      1 LLMWITQCFL 10

RESULT 2
US-09-529-206-92
; Sequence 92, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-92

Query Match      100.0%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LLMWITQCFL 10
      |||||
Db      1 LLMWITQCFL 10

RESULT 3
US-09-529-206A-92
; Sequence 92, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
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; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-92

Query Match      100.0%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LLMWITQCFL 10
      |||||
Db      1 LLMWITQCFL 10

RESULT 4
US-09-529-206B-92
; Sequence 92, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-92

Query Match      100.0%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LLMWITQCFL 10
      |||||
Db      1 LLMWITQCFL 10

RESULT 5
PCT-US00-04326-42
; Sequence 42, Application PC/TUS00004326
; GENERAL INFORMATION:
; APPLICANT: Chiari, Rita
; APPLICANT: Coulie, Pierre G.
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TYROSINE KINASE RECEPTOR EphA3 ANTIGENIC PEPTIDES
; FILE REFERENCE: L0461/7057WO
; CURRENT APPLICATION NUMBER: PCT/US00/04326
; CURRENT FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: US 60/121,170
; EARLIER FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: US 60/158,566
; EARLIER FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
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PCT-US00-04326-42

Query Match 100.0%; Score 57; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | |
Db 2 LLMWITQCFL 11

RESULT 6

PCT-US99-06875-4

; Sequence 4, Application PC/TUS9906875

; GENERAL INFORMATION:

; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
; APPLICANT: Old, Lloyd J.

; TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
; TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
; TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
; TITLE OF INVENTION: THEREFROM

; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US99/06875

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

PCT-US99-06875-4

Query Match 100.0%; Score 57; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | |
Db 2 LLMWITQCFL 11

RESULT 7

US-09-165-546A-4

; Sequence 4, Application US/09165546A

; GENERAL INFORMATION:

; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd

; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
; MHC CLASS I AND MHC CLASS II MOLECULES, AND
; USES THEREOF

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: WordPerfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/165,546A
; FILING DATE: 02-Oct-1998

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998

; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997

; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946

; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-165-546A-4

Query Match 100.0%; Score 57; DB 15; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | |
Db 2 LLMWITQCFL 11

RESULT 8

US-09-336-091-41

; Sequence 41, Application US/09336091

; GENERAL INFORMATION:

; APPLICANT: Van Snick, Jacques
; APPLICANT: Leth, Bernard

; APPLICANT: Chau, Pascal
; APPLICANT: Boon-Falleur, Thierry

; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGE-A1 PEPTIDES PRESENTED BY HLA CLASS

; TITLE OF INVENTION: II MOLECULES
; FILE REFERENCE: L0461/7063

; CURRENT APPLICATION NUMBER: US/09/336,091
; CURRENT FILING DATE: 1999-06-18

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 41

; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-336-091-41

Query Match 100.0%; Score 57; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | |
Db 2 LLMWITQCFL 11

RESULT 9

US-09-396-315-79
; Sequence 79, Application US/09396315

; GENERAL INFORMATION:

; APPLICANT: Schultz, Erwin S.

; APPLICANT: Van Snick, Jacques

; APPLICANT: Leth, Bernard

; APPLICANT: Chau, Pascal

; APPLICANT: Stroobant, Vincent

; APPLICANT: Boon-Falleur, Thierry

; APPLICANT: van der Bruggen, Pierre

; APPLICANT: Thielemans, Kris

; APPLICANT: Kurthals, Jurgen

; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES

; FILE REFERENCE: L0461/7067

; CURRENT APPLICATION NUMBER: US/09/396,315

; CURRENT FILING DATE: 1999-09-15

; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 79

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-396-315-79

Query Match 100.0%; Score 57; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | |
Db 2 LLMWITQCFL 11

RESULT 10

US-09-408-036B-4

; Sequence 4, Application US/09408036B

; GENERAL INFORMATION:

; APPLICANT: Tureci, Ozlem

; APPLICANT: Sahin, Ugur

; APPLICANT: Pfreundsckuh, Michael

; TITLE OF INVENTION: Isolated Peptides which Bind to MHC Class II Molecules and Uses Thereof

; FILE REFERENCE: LUD 5624

; CURRENT APPLICATION NUMBER: US/09/408,036B

; CURRENT FILING DATE: 1999-09-29

; PRIOR APPLICATION NUMBER: 09/344,040

; PRIOR FILING DATE: 1999-06-25

; PRIOR APPLICATION NUMBER: 09/165,546

; PRIOR FILING DATE: 1998-10-02

; NUMBER OF SEQ ID NOS: 38

; SEQ ID NO 4

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-408-036B-4

Query Match 100.0%; Score 57; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | |
Db 2 LLMWITQCFL 11

RESULT 11

US-09-440-621-1

; Sequence 1, Application US/09440621

; GENERAL INFORMATION:

; APPLICANT: Valmori, Danila

; APPLICANT: Cerottini, Jean-Charles

; APPLICANT: Romero, Pedro

; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof

; FILE REFERENCE: LUD 5629

; CURRENT APPLICATION NUMBER: US/09/440,621

; CURRENT FILING DATE: 1999-11-15

; EARLIER APPLICATION NUMBER: US 09/165,546

; EARLIER FILING DATE: 1998-10-02

; EARLIER APPLICATION NUMBER: US 09/062,422

; EARLIER FILING DATE: 1998-04-17

; EARLIER APPLICATION NUMBER: US 08/725,162

; NUMBER OF SEQ ID NOS: 10

; SEQ ID NO 1

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

US-09-440-621-1

Query Match 100.0%; Score 57; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | |
Db 2 LLMWITQCFL 11

RESULT 12

US-09-510-635A-4

; Sequence 4, Application US/09510635A

; GENERAL INFORMATION:

; APPLICANT: Bernard Leth, and Thierry Boon-Falleur

; TITLE OF INVENTION: ISOLATED GENOMIC SEQUENCES WHICH ENCODE NY-ESO-1 AND USES THEREOF

; FILE REFERENCE: LUD 5633

; CURRENT APPLICATION NUMBER: US/09/510,635A

; CURRENT FILING DATE: 2001-08-28

; PRIOR APPLICATION NUMBER: 09/165,546

; PRIOR FILING DATE: 1998-10-2

; NUMBER OF SEQ ID NOS: 18

; SEQ ID NO 4

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-510-635A-4

Query Match 100.0%; Score 57; DB 19; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | |
Db 2 LLMWITQCFL 11

RESULT 13
US-09-574-749-33
; Sequence 33, Application US/09574749
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; TITLE OF INVENTION: DEVICES
; FILE REFERENCE: C1005/7006
; CURRENT APPLICATION NUMBER: US/09/574.749
; CURRENT FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-09-574-749-33

Query Match 100.0%; Score 57; DB 19; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | | | |
Db 2 LLMWITQCFL 11

RESULT 14
US-09-676-005B-1
; Sequence 1, Application US/09676005B
; GENERAL INFORMATION:
; APPLICANT: Valmori, Danila
; APPLICANT: Cerrotini, Jean, Charels
; APPLICANT: Romero, Pedro
; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
; FILE REFERENCE: LUD 5629.2
; CURRENT APPLICATION NUMBER: US/09/676,005B
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US09/514,036
; PRIOR FILING DATE: 2000-02-05
; PRIOR APPLICATION NUMBER: US09/440,621
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 09/165,546
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: US 09/062,422
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 08/725,162
; PRIOR FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-676-005B-1

Query Match 100.0%; Score 57; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | | | |
Db 2 LLMWITQCFL 11

RESULT 15
US-09-692-401-43
; Sequence 43, Application US/09692401
; GENERAL INFORMATION:
; APPLICANT: Heidecker, Leonora
; APPLICANT: van den Eynde, Benot
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Brasseur, Francis
; TITLE OF INVENTION: MAGE-A12 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: L0461/7097
; CURRENT APPLICATION NUMBER: US/09/692,401
; CURRENT FILING DATE: 2000-10-19
; EARLIER APPLICATION NUMBER: US 60/160,374
; EARLIER FILING DATE: 1999-10-19
; EARLIER APPLICATION NUMBER: US 60/179,570
; EARLIER FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-692-401-43

Query Match 100.0%; Score 57; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | | | |
Db 2 LLMWITQCFL 11

Search completed: July 16, 2002, 07:56:35
Job time: 813 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:43:42 ; Search time 63.47 Seconds
(without alignments)
17.524 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 344541 seqs, 111227333 residues

Total number of hits satisfying chosen parameters: 344541

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	57	100.0	11	5	US-09-344-040C-130	Sequence 130, App
2	57	100.0	11	5	US-09-574-749B-33	Sequence 33, Appl
3	57	100.0	11	6	US-10-177-277-130	Sequence 130, App
4	57	100.0	28	6	US-10-117-937-255	Sequence 255, App
5	57	100.0	180	1	PCT-US02-13994-30	Sequence 30, Appl
6	57	100.0	180	5	US-09-807-512-4	Sequence 4, Appli
7	57	100.0	180	5	US-09-807-512-8	Sequence 8, Appli
8	57	100.0	180	6	US-10-117-937-74	Sequence 74, Appl
9	57	100.0	180	6	US-10-117-937-75	Sequence 75, Appl
10	57	100.0	180	6	US-10-146-473-69	Sequence 69, Appl
11	53	93.0	9	5	US-09-344-040C-123	Sequence 123, App
12	53	93.0	9	6	US-10-177-277-123	Sequence 123, App
13	47	82.5	9	1	PCT-US02-05748-24	Sequence 24, Appl
14	47	82.5	9	5	US-09-344-040C-131	Sequence 131, App
15	47	82.5	9	5	US-09-670-456A-1	Sequence 1, Appli
16	47	82.5	9	5	US-09-574-749B-34	Sequence 34, Appl
17	47	82.5	9	6	US-10-117-937-197	Sequence 197, App
18	47	82.5	9	6	US-10-177-277-131	Sequence 131, App
19	44	77.2	9	6	US-10-117-937-196	Sequence 196, App
20	38	66.7	9	1	PCT-US02-05748-25	Sequence 25, Appl
21	38	66.7	462	7	US-60-360-039-4233	Sequence 4233, Ap
22	38	66.7	996	7	US-60-382-898-110	Sequence 110, App
23	37	64.9	125	1	PCT-US02-09921-971	Sequence 971, App
24	36	63.2	176	5	US-09-935-625-10391	Sequence 10391, A
25	36	63.2	205	5	US-09-935-625-10389	Sequence 10389, A
26	36	63.2	259	5	US-09-935-625-9112	Sequence 9112, App

27	36	63.2	297	5	US-09-935-625-9111	Sequence 9111, Ap
28	36	63.2	343	5	US-09-935-625-9110	Sequence 9110, Ap
29	36	63.2	1054	7	US-60-360-039-1918	Sequence 1918, Ap
30	36	63.2	1156	5	US-09-935-625-9116	Sequence 9116, Ap
31	36	63.2	1194	5	US-09-935-625-9115	Sequence 9115, Ap
32	36	63.2	1240	5	US-09-935-625-9114	Sequence 9114, Ap
33	35	61.4	492	7	US-60-360-039-2801	Sequence 2801, Ap
34	35	61.4	635	5	US-09-540-209B-8038	Sequence 8038, Ap
35	34	59.6	86	6	US-10-117-477-67	Sequence 67, Appl
36	34	59.6	89	6	US-10-117-477-35	Sequence 35, Appl
37	34	59.6	93	6	US-10-155-881-7745	Sequence 7745, Ap
38	34	59.6	275	1	PCT-US02-10159-4	Sequence 4, Appli
39	34	59.6	275	6	US-10-112-645-4	Sequence 4, Appli
40	34	59.6	307	1	PCT-US02-09921-643	Sequence 643, App
41	34	59.6	357	6	US-10-104-047-3115	Sequence 3115, Ap
42	34	59.6	504	7	US-60-360-039-5799	Sequence 5799, Ap
43	34	59.6	1008	6	US-10-155-881-30322	Sequence 30322, A
44	33	57.9	9	1	PCT-US02-05748-26	Sequence 26, Appl
45	33	57.9	9	5	US-09-344-040C-122	Sequence 122, App

ALIGNMENTS

RESULT 1
US-09-344-040C-130
; Sequence 130, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Deter
; TITLE OF INVENTION: Expression of an SSX Gene, Peptldes Derived From Said SSX Gen
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 130
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-130

Query Match 100.0%; Score 57; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
 | | | | | | | | | |
Db 2 LLMWITQCFL 11

RESULT 2
US-09-574-749B-33
; Sequence 33, Application US/09574749B
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; TITLE OF INVENTION: DEVICES
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/09/574,749B

; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-09-574-749B-33

Query Match 100.0%; Score 57; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
|||||
Db 2 LLMWITQCFL 11
|||||

RESULT 3

US-10-177-277-130
; Sequence 130, Application US/10177277
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Expression of an Ssx Gene, Peptides Derived From Said Ssx Gene and Uses Thereof
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 130
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-130

Query Match 100.0%; Score 57; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
|||||
Db 2 LLMWITQCFL 11
|||||

RESULT 4

US-10-117-937-255
; Sequence 255, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping

; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 255
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-255

Query Match 100.0%; Score 57; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
|||||
Db 9 LLMWITQCFL 18
|||||

RESULT 5

PCT-US02-13994-30
; Sequence 30, Application PC/TUS0213994
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; APPLICANT: Cornell Research Foundation, Inc.
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; APPLICANT: Scanlan, Matthew
; APPLICANT: Stockert, Elisabeth
; TITLE OF INVENTION: COLON CANCER ANTIGEN PANEL
; FILE REFERENCE: L00461/70105WO(JRV)
; CURRENT APPLICATION NUMBER: PCT/US02/13994
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US 09/849,602
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-13994-30

Query Match 100.0%; Score 57; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
|||||
Db 158 LLMWITQCFL 167
|||||

RESULT 6

US-09-807-512-4
; Sequence 4, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Aarnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor Antigen-Lage 1

FILE REFERENCE: 0652.2200000
CURRENT APPLICATION NUMBER: US/09/807,512
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: PCT/EP99/07832
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: EP 98119583.7
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
US-09-807-512-4

Query Match 100.0%; Score 57; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
|||||
Db 158 LLMWITQCFL 167

RESULT 7
US-09-807-512-8
Sequence 8, Application US/09807512
GENERAL INFORMATION:
APPLICANT: Schrier, Peter I.
APPLICANT: Aarnoudse, Corlien
APPLICANT: Heider, Karl-Heinz
APPLICANT: Klade, Christoph
TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
TITLE OF INVENTION: Antigen-Lage 1
FILE REFERENCE: 0652.2200000
CURRENT APPLICATION NUMBER: US/09/807,512
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: PCT/EP99/07832
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: EP 98119583.7
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
US-09-807-512-8

Query Match 100.0%; Score 57; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
|||||
Db 158 LLMWITQCFL 167

RESULT 8
US-10-117-937-74
Sequence 74, Application US/10117937
GENERAL INFORMATION:
APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: SIMARD, John, J.L.
APPLICANT: DIAMOND, David, C.
APPLICANT: LIU, Liping
APPLICANT: XIE, Zhidong
TITLE OF INVENTION: EPI TOPE SEQUENCES
FILE REFERENCE: CTLIMM.027A
CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 74
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
US-10-117-937-74

Query Match 100.0%; Score 57; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
|||||
Db 158 LLMWITQCFL 167

RESULT 9
US-10-117-937-75
Sequence 75, Application US/10117937
GENERAL INFORMATION:
APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: SIMARD, John, J.L.
APPLICANT: DIAMOND, David, C.
APPLICANT: LIU, Liping
APPLICANT: XIE, Zhidong
TITLE OF INVENTION: EPI TOPE SEQUENCES
FILE REFERENCE: CTLIMM.027A
CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 75
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
US-10-117-937-75

Query Match 100.0%; Score 57; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
|||||
Db 158 LLMWITQCFL 167

RESULT 10
US-10-146-473-69
Sequence 69, Application US/10146473
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew
APPLICANT: Gout, Ivan
APPLICANT: Stockert, Elisabeth
APPLICANT: Gure, Ali
APPLICANT: Chen, Yao-Tseng
APPLICANT: Old, Lloyd
TITLE OF INVENTION: Breast Cancer Antigens
FILE REFERENCE: L00461/70130(JRV)

; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 69
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-69

Query Match 100.0%; Score 57; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
| | | | | | | | | |
Db 158 LLMWITQCFL 167

RESULT 11

US-09-344-040C-123
; Sequence 123, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-123

Query Match 93.0%; Score 53; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLMWITQCFL 10
| | | | | | | | | |
Db 1 LLMWITQCFL 9

RESULT 12

US-10-177-277-123
; Sequence 123, Application US/10177277
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21

; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-123

Query Match 93.0%; Score 53; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLMWITQCFL 10
| | | | | | | | | |
Db 1 LLMWITQCFL 9

RESULT 13

PCT-US02-05748-24
; Sequence 24, Application PC/TUS0205748
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Leturcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: PCT/US02/05748
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-05748-24

Query Match 82.5%; Score 47; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQC 8
| | | | | | | |
Db 2 LLMWITQC 9

RESULT 14

US-09-344-040C-131
; Sequence 131, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Deter
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gen
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; CURRENT APPLICATION NUMBER: US 08/851,130

;
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 131
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-131

Query Match 82.5%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQC 8
Db 2 LLMWITQC 9

RESULT 15
US-09-670-456A-1
; Sequence 1, Application US/09670456A
; GENERAL INFORMATION:
; LUD-5668-PCT
; APPLICANT: Gnjatic, Sacha
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA-C MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: LUD 5668
; CURRENT APPLICATION NUMBER: US/09/670,456A
; CURRENT FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-670-456A-1

Query Match 82.5%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQC 8
Db 2 LLMWITQC 9

Search completed: July 16, 2002, 07:58:00
Job time: 858 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:41:32 ; Search time 45.25 Seconds
(without alignments)
5.398 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %		Length	DB	ID	Description
	Score	Match				
1	57	100.0	10	4	US-09-359-503-7	Sequence 7, Appli
2	57	100.0	11	4	US-09-183-931-42	Sequence 42, Appl
3	57	100.0	11	4	US-09-359-503-4	Sequence 4, Appli
4	57	100.0	11	4	US-09-062-422-4	Sequence 4, Appli
5	57	100.0	11	4	US-08-937-263B-4	Sequence 4, Appli
6	57	100.0	11	4	US-09-166-448-79	Sequence 79, Appl
7	57	100.0	180	2	US-08-791-495-7	Sequence 7, Appli
8	57	100.0	180	2	US-08-791-495-9	Sequence 9, Appli
9	57	100.0	180	4	US-08-937-263B-8	Sequence 8, Appli
10	47	82.5	9	4	US-09-183-931-43	Sequence 43, Appl
11	47	82.5	9	4	US-09-359-503-5	Sequence 5, Appli
12	47	82.5	9	4	US-09-062-422-5	Sequence 5, Appli
13	47	82.5	9	4	US-08-937-263B-5	Sequence 5, Appli
14	47	82.5	9	4	US-09-166-448-80	Sequence 80, Appl
15	35.5	62.3	20	2	US-08-934-915-84	Sequence 84, Appl
16	35	61.4	527	1	US-08-805-814-10	Sequence 10, Appl
17	35	61.4	527	1	US-08-484-815-10	Sequence 10, Appl
18	35	61.4	527	3	US-08-888-949-10	Sequence 10, Appl
19	35	61.4	527	4	US-08-888-950-10	Sequence 10, Appl
20	35	61.4	527	4	US-09-262-758-10	Sequence 10, Appl
21	35	61.4	527	5	PCT-US95-10284-10	Sequence 10, Appl
22	33	57.9	6	4	US-09-359-503-14	Sequence 14, Appl
23	33	57.9	6	4	US-09-062-422-7	Sequence 7, Appli
24	33	57.9	6	4	US-08-937-263B-7	Sequence 7, Appli
25	33	57.9	9	4	US-09-183-931-44	Sequence 44, Appl
26	33	57.9	9	4	US-09-359-503-6	Sequence 6, Appli
27	33	57.9	9	4	US-09-062-422-6	Sequence 6, Appli

28	33	57.9	9	4	US-08-937-263B-6	Sequence 6, Appli
29	33	57.9	9	4	US-09-166-448-81	Sequence 81, Appl
30	33	57.9	49	1	US-08-118-270-202	Sequence 202, App
31	33	57.9	49	5	PCT-US93-08528-202	Sequence 202, App
32	33	57.9	498	1	US-08-496-855A-6	Sequence 6, Appli
33	33	57.9	498	2	US-08-466-589-12	Sequence 12, Appl
34	33	57.9	498	2	US-08-700-636-12	Sequence 12, Appl
35	33	57.9	498	3	US-08-467-574-12	Sequence 12, Appl
36	33	57.9	498	4	US-09-217-345-12	Sequence 12, Appl
37	33	57.9	1054	1	US-07-596-467-4	Sequence 4, Appli
38	33	57.9	1054	1	US-07-934-374-4	Sequence 4, Appli
39	33	57.9	1054	1	US-07-783-861C-2	Sequence 2, Appli
40	33	57.9	3118	2	US-08-457-273B-8	Sequence 8, Appli
41	33	57.9	3119	1	US-08-246-982A-16	Sequence 16, Appl
42	33	57.9	3119	1	US-08-453-265-16	Sequence 16, Appl
43	32.5	57.0	1239	2	US-08-937-931-2	Sequence 2, Appli
44	32.5	57.0	1239	4	US-09-285-502-2	Sequence 2, Appli
45	32.5	57.0	1239	4	US-09-709-126-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-359-503-7
; Sequence 7, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid

to


```

;
; TOPOLOGY: linear
; US-09-359-503-7
;
;
; Query Match 100.0%; Score 57; DB 4; Length 10;
; Best Local Similarity 100.0%; Pred. No. 0.00099;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 LLMWITQCFL 10
; |
; Db 1 LLMWITQCFL 10
;
;
; RESULT 2
; US-09-183-931-42
; Sequence 42, Application US/09183931C
; Patent No. 6210886
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
; FILE REFERENCE: LUD 5527.1-JEL/ES
; CURRENT APPLICATION NUMBER: US/09/183,931C
; CURRENT FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: US 09/018,422
; EARLIER FILING DATE: 1998 - 02 - 04
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 42
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
; US-09-183-931-42
;
;
; Query Match 100.0%; Score 57; DB 4; Length 11;
; Best Local Similarity 100.0%; Pred. No. 0.0011;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 LLMWITQCFL 10
; |
; Db 2 LLMWITQCFL 11
;
;
; RESULT 3
; US-09-359-503-4
; Sequence 4, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: wordPerfect
; APPLICATION DATA:
; ON NUMBER: US/09/359,503
; FILE: July 23, 1999
;
;
; to NY-
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;
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-359-503-4
;
; Query Match 100.0%; Score 57; DB 4; Length 11;
; Best Local Similarity 100.0%; Pred. No. 0.0011;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 LLMWITQCFL 10
; |
; Db 2 LLMWITQCFL 11
;
;
; RESULT 4
; US-09-062-422-4
; Sequence 4, Application US/09062422
; Patent No. 6252052
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
; TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
; TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felife & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,422
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Hanson, No. 6252052man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-062-422-4

Query Match      100.0%; Score 57; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 2 LLMWITQCFL 11

RESULT 5
US-08-937-263B-4
; Sequence 4, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-937-263B-4

Query Match      100.0%; Score 57; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
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Db 2 LLMWITQCFL 11

RESULT 6
US-09-166-448-79
; Sequence 79, Application US/09166448
; Patent No. 6291430
; GENERAL INFORMATION:
; APPLICANT: Chau, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgan
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/166,448
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-448-79

Query Match      100.0%; Score 57; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 2 LLMWITQCFL 11

RESULT 7
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
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; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-7

Query Match 100.0%; Score 57; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | | | |
Db 158 LLMWITQCFL 167

RESULT 8
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 57; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | | | |
Db 158 LLMWITQCFL 167

RESULT 9
US-08-937-263B-8

; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-08-937-263B-8

Query Match 100.0%; Score 57; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
| | | | | | | | | |
Db 158 LLMWITQCFL 167

RESULT 10
US-09-183-931-43
; Sequence 43, Application US/09183931C
; Patent No. 6210886
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
; FILE REFERENCE: LUD 5527.1-JEL/ES
; CURRENT APPLICATION NUMBER: US/09/183,931C
; CURRENT FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: US 09/018,422
; EARLIER FILING DATE: 1998 - 02 - 04
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 43
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

OTHER INFORMATION:
US-09-183-931-43

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
|||||
Db 2 LLMWITQC 9

RESULT 11

US-09-359-503-5
; Sequence 5, Application US/09359503
; Patent No. 6251603

GENERAL INFORMATION:

APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6251603man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-09-359-503-5

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
|||||

to NY

Db 2 LLMWITQC 9

RESULT 12

US-09-062-422-5
; Sequence 5, Application US/09062422
; Patent No. 6252052

GENERAL INFORMATION:

APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
APPLICANT: Old, Lloyd J.

TITLE OF INVENTION:

ANTIBODIES WHICH BIND TO NY-ESO-1
CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
THEREFROM

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,422
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6252052man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-09-062-422-5

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
|||||
Db 2 LLMWITQC 9

RESULT 13

US-08-937-263B-5
; Sequence 5, Application US/08937263B
; Patent No. 6274145

GENERAL INFORMATION:

APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
ITSELF, AND USES THEREOF

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sinn, Eric, Patent Agent
REGISTRATION NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-937-263B-5

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
Db 2 LLMWITQC 9

RESULT 14
US-09-166-448-80
Sequence 80, Application US/09166448
Patent No. 6291430
GENERAL INFORMATION:
APPLICANT: Chaux, Pascal
APPLICANT: Vantomme, Valrie
APPLICANT: Stroobant, Vincent
APPLICANT: Boon-Falleur, Thierry
APPLICANT: van der Bruggen, Pierre
APPLICANT: Thielemans, Kris
APPLICANT: Corthals, Jurgen
TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
FILE REFERENCE: L0461/7052
CURRENT APPLICATION NUMBER: US/09/166,448
CURRENT FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 80
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-166-448-80

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8

Db 2 LLMWITQC 9
RESULT 15
US-08-934-915-84
Sequence 84, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-84

Query Match 62.3%; Score 35.5; DB 2; Length 20;
Best Local Similarity 46.7%; Pred. No. 6.3;
Matches 7; Conservative 3; Mismatches 0; Indels 5; Gaps 1;

QY 1 LLMWIT----QCFL 10
Db 1 LLLWITAASAFRCFI 15

Search completed: July 16, 2002, 07:46:56
Job time: 324 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:58:07 ; Search time 14.82 Seconds
(without alignments)
64.838 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 1099

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	22	38.6	10	2	PT0289	Ig heavy chain CRD
2	20	35.1	7	2	S09652	hypothetical prote
3	20	35.1	7	2	PX0008	glucuronosyltransf
4	20	35.1	9	2	S07241	litorin - Rohde's
5	20	35.1	10	2	T17075	cytochrome-c oxida
6	19	33.3	8	2	S19288	acylase - Kluyvera
7	18	31.6	9	2	A29477	diuretic neuropept
8	18	31.6	9	2	I52974	seminal vesicle pr
9	17	29.8	5	2	B45525	actin I - malaria
10	17	29.8	7	2	S08606	hypothetical prote
11	17	29.8	9	2	A28495	conopressin G - co
12	17	29.8	9	2	S39040	lysine-conopressin
13	17	29.8	10	2	T13976	cytochrome-c oxida
14	16	28.1	8	2	A41117	acetylcholinestera
15	16	28.1	9	2	A61364	isotocin - common
16	16	28.1	9	2	PC2021	oxytocin-related p
17	16	28.1	10	2	S27873	hypothetical prote
18	16	28.1	10	2	PT0310	Ig heavy chain CRD
19	16	28.1	10	2	E41946	T-cell receptor ga
20	16	28.1	10	2	T17057	cytochrome-c oxida
21	16	28.1	10	2	T12303	cytochrome-c oxida
22	16	28.1	10	2	T14019	cytochrome-c oxida
23	16	28.1	10	2	T17060	cytochrome-c oxida
24	16	28.1	10	2	T12325	cytochrome-c oxida
25	16	28.1	10	2	T17072	cytochrome-c oxida
26	16	28.1	10	2	T12312	cytochrome-c oxida
27	15	26.3	6	2	F41946	T-cell receptor ga
28	15	26.3	7	2	A61081	tryptophyllin, bas
29	15	26.3	8	2	T13818	cytochrome oxidase

30	15	26.3	9	2	JS0302	xenopsin-related p
31	15	26.3	9	2	A60320	xenopsin-related p
32	15	26.3	9	2	PT0231	Ig heavy chain CDR
33	15	26.3	9	2	S78426	52.5K protein - sp
34	15	26.3	10	2	I44644	neurotoxin-associa
35	15	26.3	10	2	E49033	T-cell receptor ga
36	15	26.3	10	2	T13838	cytochrome-c oxida
37	15	26.3	10	2	T17066	cytochrome-c oxida
38	15	26.3	10	2	T17069	cytochrome-c oxida
39	15	26.3	10	2	T14219	cytochrome-c oxida
40	14	24.6	5	2	A60803	neuropeptide - sea
41	14	24.6	5	2	S65726	hemoglobin, extrac
42	14	24.6	6	2	PT0641	T-cell receptor be
43	14	24.6	7	2	S19630	ribosomal protein
44	14	24.6	7	2	A58512	venom heptapeptide
45	14	24.6	7	2	A34026	acetylcholinestera

ALIGNMENTS

RESULT 1
PT0289
Ig heavy chain CRD3 region (clone 4-109) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0289
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A;Reference number: PT0222; MUID:91108337
A;Accession: PT0289
A;Molecule type: DNA
A;Residues: 1-10 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 38.6%; Score 22; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLMWIT 6
|||
Db 1 LLNWIS 6

RESULT 2
S09652
hypothetical protein (aacC2 3' region) - Enterobacter cloacae (fragment)
C;Species: Enterobacter cloacae
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 08-Oct-1999
C;Accession: S09652
R;Vliegenthart, J.S.; Ketelaar-van Gaalen, P.A.G.; van de Klundert, J.A.M.
Antimicrob. Agents Chemother. 33, 1153-1159, 1989
A;Title: Nucleotide sequence of the aacC2 gene, a gentamicin resistance determinant i
A;Reference number: S09651; MUID:90024972
A;Accession: S09652
A;Molecule type: DNA
A;Residues: 1-7 <VLI>
A;Cross-references: EMBL:X51534; NID:g40878; PIDN:CAA35914.1; PID:g581034

Query Match 35.1%; Score 20; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWI 5
:::
Db 1 MIIWI 5

RESULT 3

PX0008
glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)
N;Alternate names: UDP-glucuronyltransferase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 07-Feb-1997
C;Accession: PX0008
R;Yokota, H.; Yuasa, A.; Sato, R.
J. Biochem. 104, 531-536, 1988
A;Title: Purification and properties of a form of UDP-glucuronyltransferase from liver
A;Reference number: PX0008; MUID:89197852
A;Accession: PX0008
A;Molecule type: protein
A;Residues: 1-7 <YOK>
C;Keywords: glycosyltransferase; hexosyltransferase; liver

Query Match 35.1%; Score 20; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMW 4
|||
Db 3 LLVW 6

RESULT 4
S07241
litorin - Rohde's leaf frog
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C;Accession: S07241
R;Barra, D.; Falconieri Erspamer, G.; Simmaco, M.; Bossa, F.; Melchiorri, P.; Erspamer,
FEBS Lett. 182, 53-56, 1985
A;Title: Rohdei-litorin: a new peptide from the skin of Phyllomedusa rohdei.
A;Reference number: S07241; MUID:85127560
A;Accession: S07241
A;Molecule type: protein
A;Residues: 1-9 <BAR>
C;Superfamily: gastrin-releasing peptide
C;Keywords: amidated carboxyl end; blocked amino end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 35.1%; Score 20; DB 2; Length 9;
Best Local Similarity 37.5%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 MWITQCFL 10
:| | |
Db 2 LWATGHFM 9

RESULT 5
T17075
cytochrome-c oxidase (EC 1.9.3.1) chain I - Chamaeleo fischeri mitochondrion (fragment)
C;Species: mitochondrion Chamaeleo fischeri
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999
C;Accession: T17075
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A;Title: Evolutionary shifts in three major structural features of the mitochondrial gen
A;Reference number: Z18674; MUID:97315309
A;Accession: T17075
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U82688; NID:g3603112; PID:g3603115; PIDN:AAC62275.1
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 35.1%; Score 20; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLMWI 5
|||
Db 3 LLRWL 7

RESULT 6
S19288
acylase - Kluyvera cryocrescens
C;Species: Kluyvera cryocrescens
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S19288
R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.
Biochem. J. 280, 659-662, 1991
A;Title: Chemical modification of serine at the active site of penicillin acylase fro
A;Reference number: S19288; MUID:92109664
A;Accession: S19288
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <MAR>

Query Match 33.3%; Score 19; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 MWI 5
|||
Db 3 MWV 5

RESULT 7
A29477
diuretic-neuropeptide F1 - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 31-Dec-1993
C;Accession: A29477
R;Proux, J.P.; Miller, C.A.; Li, J.P.; Carney, R.L.; Girardie, A.; Delaage, M.; Schoo
Biochem. Biophys. Res. Commun. 149, 180-186, 1987
A;Title: Identification of an arginine vasopressin-like diuretic hormone from Locusta
A;Reference number: A29477; MUID:88077077
A;Accession: A29477
A;Molecule type: protein
A;Residues: 1-9 <PRO>
A;Note: two neuropeptides, F1 and F2, were identified. F2 is an antiparallel dimer of
C;Keywords: neuropeptide

Query Match 31.6%; Score 18; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ITQC 8
|||
Db 3 ITNC 6

RESULT 8
I52974
seminal vesicle protein IV - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I52974
R;Teng, C.T.; Harris, S.E.
DNA 2, 105-111, 1983
A;Title: The seminal vesicle secretion IV gene: detection of S1 nuclease-sensitive si
A;Reference number: I52974; MUID:83261204
A;Accession: I52974
A;Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA
A:Residues: 1-9 <RES>
A:Cross-references: GB:M27324; NID:g207124; PIDN:AAA63501.1; PID:g207125
C:Genetics:
A:Gene: SVSIV

Query Match 31.6%; Score 18; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 MWITQCFL 10
| : | | |
Db 1 MKLTSFL 8

RESULT 9
B45525
actin I - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C:Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C:Accession: B45525
R;Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoenmaker, J.; Mol. Biochem. Parasitol. 35, 167-176, 1989
A:Title: Stage-specific expression and genomic organization of the actin genes of the malaria parasite Plasmodium falciparum
A:Reference number: A45525; MUID:89364996
A:Accession: B45525
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5 <WES>
A:Cross-references: GB:J03988
A:Note: The authors translated the codon GAA for residue 3 as Gly
C:Comment: The actin I gene contains no introns.

Query Match 29.8%; Score 17; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 QCF 9
: | |
Db 3 ECF 5

RESULT 10
S08606
hypothetical protein 2 estrogen receptor 5'-region - chicken
C:Species: Gallus gallus (chicken)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 18-Aug-2000
C:Accession: S08606
R;Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P. EMBO J. 5, 891-897, 1986
A:Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human oestrogen receptor
A:Reference number: S07192; MUID:86247578
A:Accession: S08606
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-7 <KRU>
A:Cross-references: EMBL:X03805; NID:g63378; PIDN:CAA27432.1; PID:g584490
C:Superfamily: unassigned leader peptides

Query Match 29.8%; Score 17; DB 2; Length 7;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 MWITQC 8
| : : |
Db 1 MFLAHC 6

RESULT 11
A28495

conopressin G - cone shell (Conus geographus)
N:Alternate names: Lys-conopressin-G
C:Species: Conus geographus (geography cone)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 25-Apr-1997
C:Accession: A28495
R;Cruz, L.J.; de Santos, V.; Zafaralla, G.C.; Ramilo, C.A.; Zeikus, R.; Gray, W.R.; O'J. Biol. Chem. 262, 15821-15824, 1987
A:Title: Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from the cone shell (Conus geographus)
A:Reference number: A92617; MUID:88058932
A:Accession: A28495
A:Molecule type: protein
A:Residues: 1-9 <CRU>
C:Superfamily: oxytocin-neurophysin
C:Keywords: amidated carboxyl end; venom
F:1-6/Disulfide bonds: #status experimental
F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 29.8%; Score 17; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CFL 10
| |
Db 1 CFI 3

RESULT 12
S39040
lysine-conopressin - Erpobdella octoculata
C:Species: Erpobdella octoculata
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
C:Accession: S39040
R;Salzet, M.; Bulet, P.; van Dorsselaer, A.; Malecha, J. Eur. J. Biochem. 217, 897-903, 1993
A:Title: Isolation, structural characterization and biological function of a lysine-conopressin from the leech Erpobdella octoculata
A:Reference number: S39040; MUID:94039146
A:Accession: S39040
A:Molecule type: protein
A:Residues: 1-9 <SAL>

Query Match 29.8%; Score 17; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CFL 10
| |
Db 1 CFI 3

RESULT 13
T13976
cytochrome-c oxidase (EC 1.9.3.1) chain I - Cnemidophorus tigris mitochondrion (fragment)
C:Species: mitochondrion Cnemidophorus tigris
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C:Accession: T13976
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J. Mol. Biol. Evol. 14, 91-104, 1997
A:Title: Two novel gene orders and the role of light-strand replication in rearrangement of the cytochrome-c oxidase gene in the lizard Cnemidophorus tigris
A:Reference number: T13976; MUID:97153826
A:Accession: T13976
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-10 <MAC>
A:Cross-references: EMBL:U71332; NID:g1753236; PID:g1753239; PIDN:AAB48274.1
C:Genetics:
A:Genome: mitochondrion
A:Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 29.8%; Score 17; DB 2; Length 10;

Best Local Similarity 57.1%; Pred. No. 5.9e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 MWITQCF 9
| | | |
Db 1 MTITRWF 7

RESULT 14
A41117
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)
C;Species: Naja naja oxiana (Asian cobra, Oxus cobra)
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 23-Jun-1993
C;Accession: A41117
R;Kreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
Prog. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo a
A;Reference number: A41117; MUID:91296772
A;Accession: A41117
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <KRE>
C;Keywords: carboxylic ester hydrolase

Query Match 28.1%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MW 4
| |
Db 4 MW 5

RESULT 15
A61364
isotocin - common carp
C;Species: Cyprinus carpio (common carp)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 20-Jun-2000
C;Accession: A61364
R;Acher, R.; Chauvet, J.; Chauvet, M.T.; Crepy, D.
Comp. Biochem. Physiol. A 14, 245-254, 1965
A;Title: Caracterisation des hormones neurohypophysaires d'un poisson osseux d'eau douce
A;Reference number: A61364
A;Accession: A61364
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <ACH>
C;Superfamily: oxytocin-neurophysin
C;Keywords: amidated carboxyl end; neuropeptide; posterior pituitary
F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.1%; Score 16; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WITQC 8
: | : |
Db 2 YISNC 6



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OM protein - protein search, using sw model

Run on: July 16, 2002, 08:02:07 ; Search time 11.74 Seconds
(without alignments)
32.981 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 349

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	35.1	9	1	LITR_PHYRO	P08946 phyllomedusa
2	18	31.6	9	1	DNFL_LOCFMI	P16339 locusta mig
3	17	29.8	9	1	CONO_CONGE	P05486 conus geogr
4	16	28.1	9	1	ISOT_CYPCA	P42993 cyprinus ca
5	16	28.1	9	1	OXYT_EISFO	P42998 eisenia foe
6	16	28.1	9	1	OXYT_RAJCL	P42994 raja clavav
7	15	26.3	5	1	UF01_MOUSE	P38639 mus musculu
8	15	26.3	9	1	MGMT_BOVIN	P29177 bos taurus
9	15	26.3	9	1	OXYA_SCYCA	P42996 scylliorhinu
10	15	26.3	9	1	OXYA_SQUAC	P42999 squalus aca
11	15	26.3	10	1	APE_CAPGI	P80474 capnocytoph
12	15	26.3	10	1	RCA_PINPS	P81084 pinus pinas
13	14	24.6	8	1	CPD1_ENTFA	P13269 enterococcu
14	14	24.6	9	1	COVN_CONVE	P83047 conus ventr
15	14	24.6	9	1	OXYT_BUFRE	P42995 bufo regula
16	14	24.6	9	1	OXYT_CYPCA	P23879 cyprinus ca
17	14	24.6	9	1	OXYT_RABIT	P32878 oryctolagus
18	14	24.6	9	1	OXYV_SQUAC	P43000 squalus aca
19	13	22.8	6	1	EI01_LITRU	P82096 litoria rub
20	13	22.8	9	1	D1_NEPNO	P24816 nephrops no
21	13	22.8	9	1	LITO_LITAU	P08945 litoria aur
22	13	22.8	10	1	GON1_PETMA	P04378 petromyzon
23	13	22.8	10	1	GON3_ONCKE	P20367 oncorhynchu
24	13	22.8	10	1	GONL_SQUAC	P27429 squalus aca
25	13	22.8	10	1	LABA_JATMU	P13270 jatrophu mu
26	13	22.8	10	1	MP2_MICOC	P81533 microplitis
27	13	22.8	10	1	NO40_TOBAC	P55962 nicotiana t
28	13	22.8	10	1	PORB_METTM	P80901 methanobact
29	12	21.1	7	1	CCF1_ENTFA	P20104 enterococcu
30	12	21.1	7	1	WWA1_ACHFUF	P35919 achatina fu
31	12	21.1	7	1	WWA2_ACHFUF	P35920 achatina fu
32	12	21.1	7	1	WWA3_ACHFUF	P35921 achatina fu
33	12	21.1	8	1	ACI_THUAL	P18691 thunnus alb

34	12	21.1	8	1	CCKN_MACEU	P30369 macropus eu
35	12	21.1	9	1	CCAP_CARMA	P38556 carcinus ma
36	12	21.1	9	1	CONO_CONST	P05487 conus stria
37	12	21.1	9	1	OXYF_SCYCA	P42997 scylliorhinu
38	12	21.1	9	1	OXYT_OCFVU	P80027 octopus vul
39	12	21.1	10	1	CAER_LITXA	P56264 litoria xan
40	12	21.1	10	1	FARP_MANSE	P18523 manduca sex
41	12	21.1	10	1	HTF1_ROMMI	P18110 romalea mic
42	12	21.1	10	1	HTF2_CARMO	P11385 carausius m
43	12	21.1	10	1	HTF_NAUCI	P10939 nauphoeta c
44	11	19.3	4	1	OCP3_OCTMI	P58649 octopus min
45	11	19.3	5	1	BPP7_BOTIN	P30425 bothrops in

ALIGNMENTS

RESULT 1						
LITR_PHYRO						
ID	LITR_PHYRO	STANDARD;	PRT;	9	AA.	
AC	P08946;					
DT	01-NOV-1988 (Rel. 09, Created)					
DT	01-FEB-1994 (Rel. 28, Last sequence update)					
DT	01-MAR-2002 (Rel. 41, Last annotation update)					
DE	Rhodei-litorin.					
OS	Phyllomedusa rohdei (Rohde's leaf frog).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;					
OC	Phyllomedusa.					
OX	NCBI_TaxID=8394;					
RN	[1]					
RP	SEQUENCE.					
RX	MEDLINE=85127560; PubMed=3838283;					
RA	Barra D., Erspamer G.F., Simmaco M., Bossa F., Melchiorri P.,					
RA	Erspamer V.;					
RT	"Rohdei-litorin: a new peptide from the skin of Phyllomedusa rohdei.";					
RL	FEBS Lett. 182:53-56(1985).					
CC	-!- SUBCELLULAR LOCATION: Secreted.					
CC	-!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN					
CC	FAMILY.					
DR	PIR; S07241; S07241.					
DR	InterPro; IPR000874; Bombesin.					
DR	Pfam; PF02044; Bombesin; 1.					
DR	PROSITE; PS00257; BOMBESIN; 1.					
KW	Bombesin family; Amidation.					
FT	MOD_RES 1 1					
FT	MOD_RES 9 9					
SQ	SEQUENCE 9 AA; 1090 MW; 4ECCC1E861ADC377 CRC64;					

Query Match 35.1%; Score 20; DB 1; Length 9;
Best Local Similarity 37.5%; Pred. No. 1e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY	3	MWITQCFL 10
	:	
Db	2	LWATGHFM 9

RESULT 2						
DNFL_LOCFMI						
ID	DNFL_LOCFMI	STANDARD;	PRT;	9	AA.	
AC	P16339;					
DT	01-AUG-1990 (Rel. 15, Created)					
DT	01-AUG-1990 (Rel. 15, Last sequence update)					
DT	15-DEC-1998 (Rel. 37, Last annotation update)					
DE	Locupressin (Diuretic neuro peptide F1/F2).					
OS	Locusta migratoria (Migratory locust).					
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;					
OC	Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;					
OC	Acridomorpha; Acridoidea; Acrididae; Locusta.					
OX	NCBI_TaxID=7004;					
RN	[1]					

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RP SEQUENCE.
RC TISSUE=Suboesophageal ganglion, and Thoracic ganglion;
RX MEDLINE=88077077; PubMed=3689410;
RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
RA Delaage M., Schooley D.A.;
RT "Identification of an arginine vasopressin-like diuretic hormone from
RT Locusta migratoria.";
RL Biochem. Biophys. Res. Commun. 149:180-186(1987).
CC -!- FUNCTION: DIURETIC HORMONE.
CC -!- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A29477; A29477.
DR InterPro; IPR000981; Neurohypophys_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Neuropeptide; Amidation.
FT DISULFID 1 6 IN F1.
FT DISULFID 1 1 INTERCHAIN (WITH C-6') (IN F2).
FT DISULFID 6 6 INTERCHAIN (WITH C-1') (IN F2).
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 31.6%; Score 18; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ITQC 8
Db 3 ITNC 6

RESULT 3
CONO_CONGE STANDARD; PRT; 9 AA.
AC P05486;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE LYS-conopressin G.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
RT peptides from Conus geographus and Conus straitus venoms.";
RL J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A28495; A28495.
DR InterPro; IPR000981; Neurohypophys_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;

Query Match 29.8%; Score 17; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 8 CFL 10
Db 1 CFI 3

RESULT 4
ISOT_CYPCA STANDARD; PRT; 9 AA.
ID ISOT_CYPCA STANDARD; PRT; 9 AA.
AC P42993;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Isotocin.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes; Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishs.";
RL Comp. Biochem. Physiol. 14:245-254(1965).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A61364; A61364.
DR InterPro; IPR000981; Neurohypophys_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match 28.1%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WITQC 8
Db 2 YISNC 6

RESULT 5
OXYT_EISFO STANDARD; PRT; 9 AA.
ID OXYT_EISFO STANDARD; PRT; 9 AA.
AC P42998;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Annetocin.
OS Eisenia foetida (Common brandling worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=94121660; PubMed=8292046;
RA Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
RT Eisenia foetida.";
RL Biochem. Biophys. Res. Commun. 198:393-399(1994).
CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
CC NEPHRIDIAL FUNCTION.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
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DR PIR; PC2021; PC2021.
DR InterPro; IPR000981; Neurohypophys_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;

Query Match 28.1%; Score 16; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CFL 10
Db 1 CFV 3

RESULT 6
OXYT_RAJCL STANDARD; PRT; 9 AA.
AC P42994;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Glumitocin.
OS Raja clavata (Thornback ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
OC Rajiformes; Rajidae; Raja.
OX NCBI_TaxID=7781;
RN [1]
RP SEQUENCE.
RX MEDLINE=66123415; PubMed=5880565;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Phylogeny of neurophyphyseal peptides: isolation of a new hormone,
glumitocin (Ser 4-Gln 8-ocytocin) present in a cartilaginous fish,
the ray (Raja clavata).";
RL Biochim. Biophys. Acta 107:393-396(1965).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohypophys_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 984 MW; 17E9C76EB455B04B CRC64;

Query Match 28.1%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WITQC 8
Db 2 YISNC 6

RESULT 7
UF01_MOUSE STANDARD; PRT; 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE.
RX TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 19 kDa.
FT NON_TER 5
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 26.3%; Score 15; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 WI 5
Db 1 WI 2

RESULT 8
MGMT_BOVIN STANDARD; PRT; 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-
methylguanine-DNA methyltransferase) (Fragment).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX TISSUE=Thymus;
RX MEDLINE=90174912; PubMed=2308822;
RA Rydberg B., Hall J., Karran P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
methyltransferase.";
RL Nucleic Acids Res. 18:17-21(1990).
CC -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY
TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE
RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS
IRREVERSIBLY INACTIVATED.
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) +
[protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein
S-methyl-L-cysteine.
CC -!- SIMILARITY: WITH SEGMENTS OF E.COLI ADA AND OGT METHYLTRANSFERASE
WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
DR InterPro; IPR001497; Methyltransf_1.
DR PROSITE; PS00374; MGMT; PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON_TER 1 1
FT ACT_SITE 9 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 26.3%; Score 15; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ITQC 8
Db 6 LTPC 9

RESULT 9

OXYA_SCYCA
ID OXYA_SCYCA STANDARD; PRT; 9 AA.
AC P42996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Asvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
fishes: asvatocin and phasvatocin, two oxytocin-like peptides
isolated from the spotted dogfish (Scyliorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohypophys_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB44404B CRC64;

Query Match 26.3%; Score 15; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 WITQC 8
:| |
Db 2 YINNC 6

RESULT 10
OXYA_SQUAC
ID OXYA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (Aspartocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohypophys_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.

FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB44404B CRC64;

Query Match 26.3%; Score 15; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 WITQC 8
:| |
Db 2 YINNC 6

RESULT 11
APE_CAPGI
ID APE_CAPGI STANDARD; PRT; 10 AA.
AC P80474;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Aminopeptidase (EC 3.4.11.-) (Fragment).
OS Capnocytophaga gingivalis.
OC Bacteria; CFB group; Flavobacteria; Flavobacteriaceae; Capnocytophaga.
OX NCBI_TaxID=1017;
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 33624;
RX MEDLINE=96118234; PubMed=8574402;
RA Spratt D.A., Greenman J., Schaffer A.G.;
RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence
factor.";
RL Microbiology 141:3087-3093(1995).
CC -!- FUNCTION: AMINOPEPTIDASE WHICH HYDROLYZES SUBSTRATES WITH FREE N-
TERMINAL AMINO ACID RESIDUES BUT NOT N-TERMINAL BLOCKED ONES.
CC OPTIMUM ACTIVITY IS MEASURED AT PH 7.5. MAY BE IMPORTANT IN THE
NUTRITION AND PATHOGENESIS OF THE ORGANISM IN THE HUMAN ORAL
CAVITY.
CC -!- COFACTOR: REQUIRES MAGNESIUM OR CALCIUM.
KW Hydrolase; Aminopeptidase; Magnesium; Calcium.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1306 MW; 00C0A6DB43772694 CRC64;

Query Match 26.3%; Score 15; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 4.1e+03;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMW 4
:| |
Db 4 MLW 6

RESULT 12
RCA_PINPS
ID RCA_PINPS STANDARD; PRT; 10 AA.
AC P81084;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable ribulose biphosphate carboxylase/oxygenase activase (RuBisCO
activase) (RA) (Water stress responsive protein 4) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=98418576; PubMed=9747804;
RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit-responsive proteins in maritime pine.";

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RL Plant Mol. Biol. 38:587-596(1998).
RN [2]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- FUNCTION: ACTIVATION OF RUBISCO (RIBULOSE-1,5-BISPHOSPHATE
CC CARBOXYLASE/OXYGENASE; EC 4.1.1.39) INVOLVES THE ATP-DEPENDENT
CC CARBOXYLATION OF THE EPSILON-AMINO GROUP OF LYSINE LEADING TO A
CC CARBAMATE STRUCTURE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Chloroplast stroma (By similarity).
CC -!- INDUCTION: BY WATER STRESS.
CC -!- SIMILARITY: BELONGS TO THE RUBISCO ACTIVASE FAMILY.
KW Chloroplast; ATP-binding.
FT NON_TER 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1171 MW; C0A506D2C72B1EA6 CRC64;

Query Match 26.3%; Score 15; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 QCFL 10
Db 3 QCEL 6

RESULT 13
CPD1_ENTFEA
ID CPD1_ENTFEA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CPD1.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, CPD1.";
RL Science 226:849-850(1984).
CC -!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOCIN PLASMID PPD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 24.6%; Score 14; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
Db 2 LVMFLS 7

RESULT 14
COVN_CONVE
ID COVN_CONVE STANDARD; PRT; 9 AA.
AC P83047;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
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DE Contryphan-Vn.
OS Conus ventricosus (Mediterranean cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=117992;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Raybaudi Massilia G., Schinina M.E., Ascenzi P., Polticelli F.;
RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean
RT vermivorous marine snail Conus ventricosus.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- TISSUE SPECIFICITY: Venom.
KW Amidation; Venom; D-amino acid.
FT DISULFID 3 9
FT MOD_RES 5 5 D-TRYPTOPHAN.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1091 MW; 8D38676323676EBA CRC64;

Query Match 24.6%; Score 14; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 WITQC 8
Db 5 WKPWC 9

RESULT 15
OXYT_BUFRE
ID OXYT_BUFRE STANDARD; PRT; 9 AA.
AC P42995;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Seritocin.
OS Bufo regularis (Leopard toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;
OC Bufo.
OX NCBI_TaxID=8390;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary neurointermediate lobe;
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophysial peptide, seritocin ([Ser5,Ile8]-oxytocin),
RT identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res. 45:482-487(1995).
CC -!- FUNCTION: DEVOID OF OXYTOCIC ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohypophys_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;

Query Match 24.6%; Score 14; DB 1; Length 9;
Best Local Similarity 33.3%; Pred. No. 1e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 CFL 10
Db 1 CYI 3

Search completed: July 16, 2002, 08:06:14
Job time: 247 sec
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 08:01:32 ; Search time 26.12 Seconds
(without alignments)
66.231 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SP TREMBL_19: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archheap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	36.8	8	2	O85406 coxiella bu
2	21	36.8	8	4	Q15890 homo sapien
3	20	35.1	8	5	Q9VRD2 drosophila
4	20	35.1	10	8	O79912 chamaeleo f
5	20	35.1	10	8	Q9G697 chamaeleo d
6	19	33.3	10	6	Q9N1X1 equus cabal
7	19	33.3	10	11	Q9ESU5 mus musculu
8	17	29.8	9	4	Q9H326 homo sapien
9	17	29.8	9	9	Q38340 lactococcu
10	17	29.8	10	2	Q48469 klebsiella
11	17	29.8	10	4	Q96QA7 homo sapien
12	17	29.8	10	8	Q9TG98 shinisauru
13	17	29.8	10	8	P92616 cnemidophor
14	16	28.1	8	8	Q94VJ4 varanus ben
15	16	28.1	8	11	Q9ET18 mus spretus
16	16	28.1	8	11	Q9ET17 mus caroli

17	16	28.1	8	11	Q9ET16	Q9etl6 mesocricetu
18	16	28.1	8	11	Q99MNO	Q99mn0 mus musculu
19	16	28.1	8	11	Q62721	Q62721 rattus norv
20	16	28.1	9	2	Q9R9C4	Q9r9c4 borrellia bu
21	16	28.1	9	4	Q9H3Y3	Q9h3y3 homo sapien
22	16	28.1	10	2	Q934S1	Q934s1 thermus the
23	16	28.1	10	5	Q25355	Q25355 locusta mig
24	16	28.1	10	5	Q25356	Q25356 locusta mig
25	16	28.1	10	6	Q9TR47	Q9tr47 bos taurus
26	16	28.1	10	8	Q92YV3	Q92yv3 dipsosaurus
27	16	28.1	10	8	Q92YU4	Q9zyu4 sceloporu
28	16	28.1	10	8	Q9ZYT2	Q9zyt2 leioccephalu
29	16	28.1	10	8	P92707	P92707 platysaurus
30	16	28.1	10	8	P92632	P92632 eremias gra
31	16	28.1	10	8	O79891	O79891 crotophytus
32	16	28.1	10	8	O79894	O79894 gambelia wi
33	16	28.1	10	8	O79909	O79909 sauromalus
34	16	28.1	10	8	Q9T8G5	Q9t8g5 liolaemus o
35	16	28.1	10	8	Q9B4X0	Q9b4x0 notophthalm
36	16	28.1	10	8	Q958K9	Q958k9 rana boylli
37	16	28.1	10	11	Q61807	Q61807 mus musculu
38	15	26.3	8	12	Q9E8Q4	Q9e8q4 beet soil-b
39	15	26.3	8	12	Q9DSN5	Q9dsn5 beet soil-b
40	15	26.3	9	4	Q99887	Q99887 homo sapien
41	15	26.3	9	8	Q94VI8	Q94vi8 varanus ere
42	15	26.3	9	8	Q94VH4	Q94vh4 varanus gla
43	15	26.3	9	8	Q94VE1	Q94ve1 varanus mer
44	15	26.3	9	8	Q94VD8	Q94vd8 varanus nil
45	15	26.3	9	9	Q38366	Q38366 bacterioph

ALIGNMENTS

RESULT 1
O85406
ID O85406 PRELIMINARY; PRT; 8 AA.
AC O85406;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 1.0 KDA PROTEIN (FRAGMENT).
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
OC Coxiella group; Coxiella.
OX NCBI_TaxID=777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NINE MILE PHASE I;
RX MEDLINE=98348442; PubMed=9683477;
RA Willems H., Jaeger C., Baljer G.;
RT "Physical and genetic map of the obligate intracellular bacterium Coxiella burnetii."
RL J. Bacteriol. 180:3816-3822(1998).
DR EMBL; AF064963; AAD09947.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 8 AA; 993 MW; 046B5AA453772727 CRC64;

Query Match 36.8%; Score 21; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 5.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMW 4
||:|
Db 1 LLLW 4

RESULT 2
Q15890
ID Q15890 PRELIMINARY; PRT; 8 AA.
AC Q15890;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (CLONE XP19G12A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32083; AAA73880.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;

Query Match 36.8%; Score 21; DB 4; Length 8;
Best Local Similarity 37.5%; Pred. No. 5.6e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 2; Gaps 1;

QY 4 WI--TQCF 9
Db 1 WVSCSQCY 8

RESULT 3
Q9VRD2
ID Q9VRD2 PRELIMINARY; PRT; 8 AA.
AC Q9VRD2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CG11666 PROTEIN.
GN CG11666.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielson A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003569; AAF50870.1; -.
DR FlyBase; FBgn0040648; CG11666.
SQ SEQUENCE 8 AA; 1062 MW; ED11B5B044004376 CRC64;

Query Match 35.1%; Score 20; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MWI 5
Db 1 MWI 3

RESULT 4
O79912
ID O79912 PRELIMINARY; PRT; 10 AA.
AC O79912;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Chamaeleo fischeri.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
OX NCBI_TaxID=51755;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97315309; PubMed=9169559;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Evolutionary shifts in three major structural features of the
RT mitochondrial genome among iguanian lizards.";
RL J. Mol. Evol. 44:660-674(1997).
DR EMBL; U82688; AAC62275.1; -.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1319 MW; 5E218E2733640727 CRC64;

Query Match 35.1%; Score 20; DB 8; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLMWI 5
Db 3 LLRWL 7

RESULT 5
Q9G697
ID Q9G697 PRELIMINARY; PRT; 10 AA.
AC Q9G697;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).

GN COI.
OS Chamaeleo dilepis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
OX NCBI_TaxID=91908;
RN [1]
RP SEQUENCE FROM N.A.
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128460; AAG00617.1; -.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1319 MW; 5E218E2733640727 CRC64;

Query Match 35.1%; Score 20; DB 8; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLMWI 5
|||
Db 3 LLRWL 7

RESULT 6
Q9N1X1 PRELIMINARY; PRT; 10 AA.
AC Q9N1X1;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE ALCOHOL DEHYDROGENASE 3 (FRAGMENT).
GN ADH3.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20082971; PubMed=10613847;
RA Caetano A.R., Shieh Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA Bowling A.T., Murray J.D.;
RT "A comparative gene map of the horse (Equus caballus).";
RL Genome Res. 9:1239-1249(1999).
DR EMBL; AF134056; AAF31299.1; -.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1144 MW; C4EA25676B02D6DD CRC64;

Query Match 33.3%; Score 19; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.3e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 WIT 6
|||
Db 8 WVT 10

RESULT 7
Q9ESU5 PRELIMINARY; PRT; 10 AA.
ID Q9ESU5
AC Q9ESU5;

DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE FAS DEATH RECEPTOR (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HE;
RX MEDLINE=20127858; PubMed=10660538;
RA Munsch D., Watanabe-Fukunaga R., Bourdon J.C., Nagata S., May E.,
RA Yonish-Rouach E., Reisdorf P.;
RT "Human and mouse Fas (APO-1/CD95) death receptor genes each contain a
RT p53-responsive element that is activated by p53 mutants unable to
RT induce apoptosis.";
RL J. Biol. Chem. 275:3867-3872(2000).
DR EMBL; AF282865; AAG02410.1; -.
KW Receptor.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1242 MW; 22145E32CDC37043 CRC64;

Query Match 33.3%; Score 19; DB 11; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMWI 5
:|||
Db 1 MLWI 4

RESULT 8
Q9H326 PRELIMINARY; PRT; 9 AA.
ID Q9H326
AC Q9H326;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE NAD+-DEPENDENT ISOCITRATE DEHYDROGENASE 3 ALPHA SUBUNIT
DE (FRAGMENT).
GN IDH3A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.-O., Koh H.-J., Jo S.-H., Son M.-K., Huh T.-L.;
RT "Structural and functional characterization of the human NAD+-
RT dependent isocitrate dehydrogenase alpha subunit promoter.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157515; AAG43379.1; -.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 960 MW; C91CB0437DC7687D CRC64;

Query Match 29.8%; Score 17; DB 4; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 WITQ 7
||::|
Db 6 WISK 9

RESULT 9
Q38340 PRELIMINARY; PRT; 9 AA.
ID Q38340
AC Q38340;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)


```
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF PROTEIN (FRAGMENT).
GN ORF.
OS Lactococcus phage 936.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=39838;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96084945; PubMed=7489923;
RA Waterfield N.R., Lepage R.W., Wilson P.W., Wells J.M.;
RT "The isolation of lactococcal promoters and their use in investigating
RT bacterial luciferase synthesis in Lactococcus lactis.";
RL Gene 165:9-15(1995).
DR EMBL; Z48181; CAA88226.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1054 MW; 7098B2CEA6D3372B CRC64;

Query Match 29.8%; Score 17; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 MWITQC 8
| : ||
Db 1 MELKQC 6

RESULT 10
Q48469
ID Q48469 PRELIMINARY; PRT; 10 AA.
AC Q48469;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NITROGENASE (FRAGMENT).
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83246546; PubMed=6306580;
RA Shen S.C., Xue Z.T., Kong Q.T., Wu Q.L.;
RT "An open reading frame upstream from the nifH gene of Klebsiella
RT pneumoniae.";
RL Nucleic Acids Res. 11:4241-4250(1983).
DR EMBL; X01006; CAA25501.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1173 MW; B130695DDEA6C406 CRC64;

Query Match 29.8%; Score 17; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 MWITQC 8
| : ||
Db 1 MTMRQC 6

RESULT 11
Q96QA7
ID Q96QA7 PRELIMINARY; PRT; 10 AA.
AC Q96QA7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE BA151A2.1 (CDC42 GUANINE EXCHANGE FACTOR (GEF) 9 (COLLYBISTIN, PEM-2,
DE HPEM-2, KIAA0424)) (FRAGMENT).
GN ARHGEF9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Whitehead S.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL451106; CAC88408.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1122 MW; 39925CB878640043 CRC64;

Query Match 29.8%; Score 17; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.5e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMWI 5
| : ||
Db 1 MQWI 4

RESULT 12
Q9TG98
ID Q9TG98 PRELIMINARY; PRT; 10 AA.
AC Q9TG98;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Shinisaurus crocodilurus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Shinisauridae;
OC Shinisaurus.
OX NCBI_TaxID=52224;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99343613; PubMed=10413621;
RA Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
RA Papenfuss T.J.;
RT "Molecular phylogenetics, tRNA evolution, and historical biogeography
RT in anguid lizards and related taxonomic families.";
RL Mol. Phylogenet. Evol. 12:250-272(1999).
DR EMBL; AF085604; AAD51502.1; -.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1290 MW; 1CEE80C9D36411A0 CRC64;

Query Match 29.8%; Score 17; DB 8; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 MWITQCF 9
| : || : |
Db 1 MTITRWF 7

RESULT 13
P92616
ID P92616 PRELIMINARY; PRT; 10 AA.
AC P92616;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Cnemidophorus tigris.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Teiioidea;
OC Teiidae; Cnemidophorus.
OX NCBI_TaxID=52180;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=97153826; PubMed=9000757;
RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
RT "Two novel gene orders and the role of light-strand replication in
RT rearrangement of the vertebrate mitochondrial genome.";
RL Mol. Biol. Evol. 14:91-104(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
RT structures of mitochondrial transfer RNAs.";
RL Mol. Biol. Evol. 14:30-39(1997).
DR EMBL; U71332; AAB48274.1; -.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1290 MW; 1CEE80C9D36411A0 CRC64;

Query Match 29.8%; Score 17; DB 8; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 MWITQCF 9
   | | |
Db 1 MTITRWF 7

RESULT 14
Q94VJ4
ID Q94VJ4 PRELIMINARY; PRT; 8 AA.
AC Q94VJ4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Varanus bengalensis nebulosis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169827;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RT Cladistics 17:0-0(2001).
DR EMBL; AF407492; AAL10031.1; -.
KW Mitochondrion.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1053 MW; E8B5B9C733640056 CRC64;

Query Match 28.1%; Score 16; DB 8; Length 8;
Best Local Similarity 20.0%; Pred. No. 5.6e+05;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLMWI 5
   : : |
Db 1 MIRWL 5

RESULT 15
Q9ET18
ID Q9ET18 PRELIMINARY; PRT; 8 AA.
AC Q9ET18;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE NEUROPEPTIDE Y (FRAGMENT).
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
RA Taylor B.A., Wnek C., Phillips S.J.;
RT "Multiple obesity QTLs identified in an intercross between the NZO
RT (New Zealand obese) and the SM (small) mouse strains.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF286200; AAG01474.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1033 MW; 297685A76AAB1734 CRC64;

Query Match 28.1%; Score 16; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MW 4
   | |
Db 7 MW 8

Search completed: July 16, 2002, 08:05:41
Job time: 249 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:48:27 ; Search time 26.34 Seconds
(without alignments)
42.169 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 135323

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802: *
1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT: *
2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT: *
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4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT: *
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8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT: *
9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT: *
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12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT: *
13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT: *
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17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT: *
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19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT: *
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT: *
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT: *
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	AA1980003	Human cancer antig
2	57	100.0	10	AA1982434	Human tumour antig
3	53	93.0	9	AA1980032	Human cancer antig
4	53	93.0	9	AA1980033	Human cancer antig
5	53	93.0	9	AA1987956	NY-ESO-1 derived p
6	53	93.0	9	AA1987170	Cancer testis tumo
7	53	93.0	9	AA1987171	Cancer testis tumo
8	53	93.0	9	AA1989902	Human NY-ESO-1 HLA
9	53	93.0	9	AA1989903	Human NY-ESO-1 HLA
10	53	93.0	10	AA1980006	Human cancer antig
11	53	93.0	10	AA1985307	HLA-A2 binding NY-

12	47	82.5	9	19	AA1982586	Cancer associated
13	47	82.5	9	20	AA1981762	Exemplary antigeni
14	47	82.5	9	21	AA1980703	Antigenic peptide
15	47	82.5	9	21	AA19822791	NY-ESO-1 peptide e
16	47	82.5	9	21	AA19802631	Tumour associated
17	47	82.5	9	21	AA19878470	NY-ESO-1 derived p
18	47	82.5	9	21	AA1982432	Human tumour antig
19	47	82.5	9	22	AA1987166	Cancer testis tumo
20	47	82.5	9	22	AA19806850	Human NY-ESO-1 ant
21	47	82.5	9	22	AA1985299	HLA-A2 binding NY-
22	47	82.5	9	22	AA1982120	NY-ESO-1 human leu
23	47	82.5	9	22	AA19801537	Cytolytic T cell 1
24	47	82.5	9	22	AA1982017	HLA- binding pepti
25	47	82.5	9	22	AA19869948	Human NY-ESO-1 Ctl
26	47	82.5	9	22	AA19831329	Exemplary antigen
27	47	82.5	10	22	AA1985309	HLA-A2 binding NY-
28	47	82.5	10	22	AA1985310	HLA-A2 binding NY-
29	44	77.2	10	20	AA19806005	Human cancer antig
30	44	77.2	10	22	AA19807778	Human NY ESO-1 epi
31	44	77.2	10	22	AA1985313	HLA-A2 binding NY-
32	38	66.7	9	22	AA1985303	HLA-A2 binding NY-
33	38	66.7	9	22	AA1985304	HLA-A2 binding NY-
34	38	66.7	9	22	AA1985305	HLA-A2 binding NY-
35	38	66.7	9	22	AA1985306	HLA-A2 binding NY-
36	38	66.7	9	22	AA1985308	HLA-A2 binding NY-
37	38	66.7	9	22	AA1985315	HLA-A2 binding NY-
38	38	66.7	9	22	AA1985316	HLA-A2 binding NY-
39	38	66.7	10	22	AA1985311	HLA-A2 binding NY-
40	38	66.7	10	22	AA1985312	HLA-A2 binding NY-
41	38	66.7	10	22	AA1985314	HLA-A2 binding NY-
42	34	59.6	9	22	AA1985317	HLA-A2 binding NY-
43	33.5	58.8	10	20	AA19806029	Human cancer antig
44	33	57.9	6	19	AA1982588	Cancer associated
45	33	57.9	6	21	AA1982441	Human tumour antig

ALIGNMENTS

RESULT 1
AA19806003
ID AA19806003 standard; Peptide; 10 AA.
XX
AC AA19806003;
XX
DT 16-AUG-1999 (first entry)
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO19818206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.
XX

PT Cancer antigen NY ES01/CAG-3
XX Example 10; Page 42; 88pp; English.
PS
XX
CC This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC The present peptide (ranked 16) corresponds to amino acid residues
CC 158-167 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 57; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 1 llmwitqcfl 10
| | | | | | | |

RESULT 2
AAY52434
ID AAY52434 standard; peptide; 10 AA.
XX
AC AAY52434;
XX
DT 15-FEB-2000 (first entry)
XX
DE Human tumour antigen NY-ESO-1 peptide #7.
XX
KW Cancer; tumour; antigen; MHC; major histocompatibility complex; Class I;
KW T-cell; cytotoxic; stimulation; proliferation; treatment;
KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW lymphoma.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9953938-A1.
XX
PD 28-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US06875.
XX
PR 17-APR-1998; 98US-0062422.
PR 02-OCT-1998; 98US-0165546.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX
DR WPI; 2000-038483/03.
XX
PT Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes -
XX
PS Claim 55; Page 20; 49pp; English.
XX

CC Peptides #4-#7 (AAY52431-Y52434) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (AAY52430) which contain the motif LLMWIT
CC (AAY52441). These sequences can bind to MHC (major histocompatibility
CC Class I HLA-A2 molecules, thereby stimulating proliferation of
CC cytotoxic T-cells. cDNA encoding NY-ESO-1 was initially isolated
CC from an oesophagus squamous cell cancer cDNA library. Tissue
CC localisation studies revealed it to be expressed at high levels
CC in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC These NY-ESO-1-derived peptides may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of
CC cancers (such as melanoma, breast cancer, prostate cancer, lung
CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 57; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 1 llmwitqcfl 10
| | | | | | | |

RESULT 3
AAY06032
ID AAY06032 standard; Peptide; 9 AA.
XX
AC AAY06032;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ES01/CAG-3
XX
PS Example 10; Page 43; 88pp; English.
XX
CC This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY06018-47) were identified.
CC The present peptide (ranked 15) corresponds to amino acid residues
CC 159-167 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent

CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX Sequence 9 AA;
SQ

Query Match 93.0%; Score 53; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMWITQCF 10
| | | | |
Db 1 lmwitqcf 9

RESULT 4
AAY06033
ID AAY06033 standard; Peptide; 9 AA.
XX
AC AAY06033;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3
XX
PS Example 10; Page 43; 88pp; English.
XX

This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY06018-47) were identified.
CC The present peptide (ranked 16) corresponds to amino acid residues
CC 158-166 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived

CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX Sequence 9 AA;
SQ

Query Match 93.0%; Score 53; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
| | | | |
Db 1 llmwitqcf 9

RESULT 5
AAY79756
ID AAY79756 standard; Peptide; 9 AA.
XX
AC AAY79756;
XX
DT 10-MAY-2000 (first entry)
XX
DE NY-ESO-1 derived peptide #12.
XX
KW Cancer; SSX family; SSX-1; SSX-2; SSX-3; SSX-4; SSX-5; NY-ESO-1;
KW HLA binding; human leukocyte antigen; cytolytic T cell; CTL;
KW cytostatic; melanoma; synovial sarcoma.
XX
OS Homo sapiens.
XX
PN WO200000824-A1.
XX
PD 06-JAN-2000.
XX
PF 25-JUN-1999; 99WO-US14493.
XX
PR 26-JUN-1998; 98US-0105839.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Tureci O, Sahin U, Pfreundschuh M, Rammensee G, Stevanovic S;
PI Chen Y, Gure A, Old LJ;
XX
DR WPI; 2000-170933/15.
XX
PT Determining the possible presence of breast, endometrial, colorectal,
PT lung, bladder or head-neck cancer -
XX
PS Example 13; Page 26; 40pp; English.
XX

A method has been developed for determining the possible presence of a
CC cancer, which is not melanoma or synovial sarcoma. The method comprises
CC assaying a sample taken from the subject to determine the expression of
CC an SSX gene, and determining the expression as a determination of the
CC possible presence of cancer. Expression of SSX1 gene indicates possible
CC presence of breast, endometrial, colorectal, lung, bladder or head-neck
CC cancer. These cancers are also detected by SSX2 and SSX4 gene
CC expression. SSX2 gene expression additionally indicates possible presence
CC of lymphoma, renal cell cancer, glioma and prostate cancer. Expression
CC of SSX4 gene also indicates possible presence of ovarian or stomach
CC cancer. SSX5 gene expression indicates the same cancers as SSX1, except
CC breast cancer. Determining expression of SSX gene can be used to monitor
CC progress of melanoma or synovial sarcoma, which is not cancer. The
CC SSX-derived peptide complex stimulates proliferation of cytolytic T
CC cells. This is useful for treating cancer, especially melanoma. AAY78464
CC to AAY78468 represent specifically claimed HLA binding peptides for use
CC in the method of the invention. AAZ88452 to AAZ88465 represent PCR
CC primers used in the isolation of SSX genes in the exemplification of the
CC present invention. AAY78469 to AAY78500, and AAY79684 to AAY79762

```
CC represent peptides derived from SSX proteins or NY-ESO-1, which are used
CC in the exemplification of the present invention.
XX
SQ Sequence 9 AA;

Query Match 93.0%; Score 53; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMWITQCFL 10
Db 1 lmwitqcfl 9

RESULT 6
AAG67170
ID AAG67170 standard; peptide; 9 AA.
XX
AC AAG67170;
XX
DT 13-NOV-2001 (first entry)
XX
DE Cancer testis tumour antigen NY-ESO-1 derived peptide.
XX
KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW HLA; HLA binding peptide; major histocompatibility complex; MHC;
KW tumour; cancer; testis tumour.
XX
OS Homo sapiens.
XX
PN WO200162917-A1.
XX
PD 30-AUG-2001.
XX
PF 22-JAN-2001; 2001WO-US02126.
XX
PR 22-FEB-2000; 2000US-0510635.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Lethe B, Boon-Falleur T;
XX
DR WPI; 2001-550091/61.
XX
PT Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful
PT for diagnosing testicular tumours -
XX
PS Example 13; Page 26; 50pp; English.
XX
CC AAG67169-AAG67206 represent peptides which are derived from cancer
CC testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptides
CC bind to human leukocyte antigens (HLAs). NY-ESO-1 is a molecule that
CC is processed to at least one human leukocyte antigen (HLA) binding
CC peptide, which binds to Class I and Class II major histocompatibility
CC complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis,
CC but not normal colon, kidney, liver or brain tissue. The presence or
CC level of expression of NY-ESO-1 may be assayed for the diagnosis of
CC cancer, especially testis tumours.
XX
SQ Sequence 9 AA;

Query Match 93.0%; Score 53; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
Db 1 llmwitqcf 9

RESULT 7
WO200107917-A1.
```

```
AAG67171
ID AAG67171 standard; peptide; 9 AA.
XX
AC AAG67171;
XX
DT 13-NOV-2001 (first entry)
XX
DE Cancer testis tumour antigen NY-ESO-1 derived peptide.
XX
KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW HLA; HLA binding peptide; major histocompatibility complex; MHC;
KW tumour; cancer; testis tumour.
XX
OS Homo sapiens.
XX
PN WO200162917-A1.
XX
PD 30-AUG-2001.
XX
PF 22-JAN-2001; 2001WO-US02126.
XX
PR 22-FEB-2000; 2000US-0510635.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Lethe B, Boon-Falleur T;
XX
DR WPI; 2001-550091/61.
XX
PT Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful
PT for diagnosing testicular tumours -
XX
PS Example 13; Page 26; 50pp; English.
XX
CC AAG67169-AAG67206 represent peptides which are derived from cancer
CC testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptides
CC bind to human leukocyte antigens (HLAs). NY-ESO-1 is a molecule that
CC is processed to at least one human leukocyte antigen (HLA) binding
CC peptide, which binds to Class I and Class II major histocompatibility
CC complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis,
CC but not normal colon, kidney, liver or brain tissue. The presence or
CC level of expression of NY-ESO-1 may be assayed for the diagnosis of
CC cancer, especially testis tumours.
XX
SQ Sequence 9 AA;

Query Match 93.0%; Score 53; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMWITQCFL 10
Db 1 lmwitqcfl 9

RESULT 8
AAB69902
ID AAB69902 standard; Peptide; 9 AA.
XX
AC AAB69902;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA binding motif #2.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
```


XX 01-FEB-2001.
XX 14-JUL-2000; 2000WO-US19220.
PF XX
XX 23-JUL-1999; 99US-0359503.
XX (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX WPI; 2001-182822/18.
DR Method useful for determining the status (e.g. progression, regression
XX or stability of the disease) of a cancerous condition, involves
XX determining the levels of NY-ESO-1 specific antibodies in a sample
PA taken from a patient -
PA
XX Example 14; Page 24; 50pp; English.
PS The present sequence is given in a specification relating to a method
XX for determining the status of a cancerous condition in a patient
XX with a tumour that expresses NY-ESO-1. The method comprises assaying a
XX sample taken from the patient for antibodies that specifically bind to
XX the NY-ESO-1 and comparing the value obtained to a prior value obtained
XX from assay of a prior sample taken from the patient. Any difference
XX between the values is indicative of a change in status of the cancerous
XX condition. The method is useful for determining whether a cancerous
XX condition is progressing, regressing or remaining stable, in particular
XX in patients receiving treatment for a melanoma, adenocarcinoma,
XX non-small cell lung carcinoma or bladder carcinoma.
XX Sequence 9 AA;
SQ
Query Match 93.0%; Score 53; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. NO. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLMWITQCF 9
Db | | | | | | | |
1 llmwitqcf 9
RESULT 9
AAB69903
ID AAB69903 standard; Peptide; 9 AA.
XX
AC AAB69903;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA binding motif #3.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US19220.
XX
PR 23-JUL-1999; 99US-0359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.

XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX WPI; 2001-182822/18.
DR Method useful for determining the status (e.g. progression, regression
XX or stability of the disease) of a cancerous condition, involves
XX determining the levels of NY-ESO-1 specific antibodies in a sample
PA taken from a patient -
PA
XX Example 14; Page 24; 50pp; English.
PS The present sequence is given in a specification relating to a method
XX for determining the status of a cancerous condition in a patient
XX with a tumour that expresses NY-ESO-1. The method comprises assaying a
XX sample taken from the patient for antibodies that specifically bind to
XX the NY-ESO-1 and comparing the value obtained to a prior value obtained
XX from assay of a prior sample taken from the patient. Any difference
XX between the values is indicative of a change in status of the cancerous
XX condition. The method is useful for determining whether a cancerous
XX condition is progressing, regressing or remaining stable, in particular
XX in patients receiving treatment for a melanoma, adenocarcinoma,
XX non-small cell lung carcinoma or bladder carcinoma.
XX Sequence 9 AA;
SQ
Query Match 93.0%; Score 53; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. NO. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 LMWITQCFL 10
Db | | | | | | | |
1 lmwitqcf 9
RESULT 10
AAY06006
ID AAY06006 standard; Peptide; 10 AA.
XX
AC AAY06006;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3
XX
PS Example 10; Page 42; 88pp; English.

XX This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.
CC The present peptide (ranked 19) corresponds to amino acid residues
CC 157-166 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see AAY05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.

XX Sequence 10 AA;

Query Match 93.0%; Score 53; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
Db 2 llmwitqcf 10

RESULT 11
AAB85307
ID AAB85307 standard; peptide; 10 AA.
XX AAB85307;
XX 17-SEP-2001 (first entry)
XX HLA-A2 binding NY-ESO-1 peptide (residues 157-166).
XX NY-ESO-1; human leukocyte antigen; HLA; lysis; cytolytic T cell; CTL;
KW HLA-A2; T-cell sorter; tumor; immune tetramer.
XX Homo sapiens.
XX WO200136453-A2.
XX 25-MAY-2001.
XX 08-NOV-2000; 2000WO-US42010.
XX 15-NOV-1999; 99US-0440621.
PR 25-FEB-2000; 2000US-0514036.
PR 29-SEP-2000; 2000US-0676005.
XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYOX-) UNIV OXFORD.
XX Valmori D, Cerottini J, Romero P, Cerundolo V;
XX WPI; 2001-451454/48.
XX Novel isolated NY-ESO-1 nonapeptide useful for determining if a cell
PT presents human leukocyte antigen-A2 molecule on its surface, binds to
PT human leukocyte antigen molecules and provokes lysis by cytolytic T
PT cells -
XX Example 11; Page 11; 38pp; English.
XX The invention provides NY-ESO-1 peptide derivatives which bind to human
CC leukocyte antigen (HLA) molecules and provokes lysis by cytolytic T cells
CC (CTLs). The NY-ESO-1 nonapeptide is of formula SLLMWITQX, where X is an
CC amino acid having an uncharged polar side chain. The NY-ESO-1 peptide

CC derivatives are useful for determining if a cell presents an HLA-A2
CC molecule on its surface, by contacting a sample containing the cell with
CC the peptide or its derivative, and determining binding between them,
CC where the binding is indicative of HLA-A2 on the surface of the cell.
CC The NY-ESO-1 peptides and analogues are useful therapeutically, for
CC administration to a patient who is HLA-A2 positive and expresses NY-ESO-1
CC in connection with the pathology, as well as diagnostically, i.e. to
CC determine if HLA-A2 positive cells are present, or if relevant CTLs are
CC present. They are also useful for determining the presence of CTLs in a
CC sample. The peptides are useful as T-cell sorters, when incorporated into
CC immune tetramers. The present sequence represents a NY-ESO-1 peptide
CC that can bind to HLA-A2 molecule.

XX Sequence 10 AA;

Query Match 93.0%; Score 53; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
Db 2 llmwitqcf 10

RESULT 12
AAW62586
ID AAW62586 standard; Peptide; 9 AA.
XX AAW62586;
XX 17-SEP-1998 (first entry)
XX Cancer associated antigen peptide.
XX Cancer associated antigen; NY-ESO-1; regression; progression; onset;
KW cancer; treatment; diagnosis.
XX Synthetic.
OS Homo sapiens.
XX WO9814464-A1.
XX 09-APR-1998.
XX 15-SEP-1997; 97WO-US16335.
XX 03-OCT-1996; 96US-0725182.
XX (LUDW-) LUDWIG INST CANCER RES.
XX Chen Y, Drijfhout JW, Gure A, Jager E, Knuth A;
PI Old LJ, Scanlan M;
XX WPI; 1998-286417/25.
XX New isolated cancer associated antigen - is used to develop products
PT for the diagnosis and treatment of cancers and for monitoring cancer
PT therapy
XX Claim 33; Page 17; 49pp; English.
XX Peptides AAW62585-87 are derived from cancer associated antigen
CC NY-ESO-1, and are stimulators of cytotoxic T-cells. The specification
CC describes a method for determining regression, progression of onset of a
CC cancerous condition, comprising monitoring a sample from a patient
CC with the cancerous condition for a parameter selected from NY-ESO-1
CC protein, a peptide derived from NY-ESO-1 protein and cytolytic
CC T cells specific for the peptide and an MHC molecule with which it
CC non-covalently complexes. Methods for the treatment of a cancerous
CC condition are also described. The NY-ESO-1 protein and peptides derived
CC from it can be used for diagnosis and treatment of cancers and to
CC monitor the efficacy of a therapeutic regime.

```
XX SQ Sequence 9 AA;
Query Match 82.5%; Score 47; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
Db 2 llmwitqc 9

RESULT 13
AAY01762
ID AAY01762 standard; Peptide; 9 AA.
XX AC AAY01762;
XX DT 25-JUN-1999 (first entry)
XX DE Exemplary antigenic peptide derived from NY-ESO-1.
XX KW MAGE-3; tumour associated gene; human leukocyte antigen Class II;
KW autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;
KW osteosarcoma; leukemia; carcinoma.
XX OS Homo sapiens.
XX PN WO9914326-A1.
XX PD 25-MAR-1999.
XX PF 04-SEP-1998; 98WO-US18601.
XX PR 12-SEP-1997; 97US-0928615.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI (UYVR-) UNIV VRIJE BRUSSEL.
XX PI Boon-Falleur T, Chaux P, Corthals J, Heirman C;
PI Luiten R, Stroobant V, Thielemans K, Van Der Bruggen P;
DR WPI; 1999-244031/20.
XX PT Isolated peptides that bind to human leukocyte antigen class II
XX molecules
XX PS Disclosure; Page 29; 88pp; English.
XX CC The present sequence represents an exemplary tumour associated peptide
XX antigen. The specification describes a MAGE-3 tumour associated gene.
XX CC Peptides (AAY01721-25) that bind human leukocyte antigen (HLA) Class II
XX molecules can be derived from the MAGE-3 protein. These peptides and
XX autologous CD4+ cells that bind to a complex of MAGE-3 peptide
XX and HLA Class II, are used to treat MAGE-3 related diseases,
XX particularly cancers (e.g. melanoma, osteosarcoma, leukemia and
XX various forms of carcinoma). The peptides are also used to produce
XX specific antibodies. Detection of of the peptides, e.g. in binding
XX assays, particularly with antibodies, is used for diagnosis of such
XX diseases.
XX SQ Sequence 9 AA;
Query Match 82.5%; Score 47; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
Db 2 llmwitqc 9
```

```
RESULT 14
AAB08703
ID AAB08703 standard; Peptide; 9 AA.
XX AC AAB08703;
XX DT 02-JAN-2001 (first entry)
XX DE Antigenic peptide from tumour rejection antigen NY-ESO-1.
XX KW EphA3; HLA class II-binding peptide; human leukocyte antigen; antigen;
KW CD4+ T lymphocyte; tumour associated gene; vaccine.
XX OS Homo sapiens.
XX PN WO200050589-A1.
XX PD 31-AUG-2000.
XX PF 18-FEB-2000; 2000WO-US04326.
XX PR 22-FEB-1999; 99US-0121170.
XX PR 08-OCT-1999; 99US-0158566.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Chiari R, Coulie P, Boon-Falleur T;
XX DR WPI; 2000-572089/53.
XX PT Novel tyrosine kinase receptor, EphA3 human leukocyte antigen (HLA)
XX class II binding peptide and nucleic acid encoding the receptor, useful
XX for diagnosing and treating conditions characterized by expression of
XX EphA3 gene
XX PS Disclosure; Page 36; 107pp; English.
XX CC AAB08668-B08704 represent antigenic peptides characteristic of tumours.
XX The peptides may be combined in vaccines with a human EphA3 HLA (human
XX leukocyte antigen) class II-binding peptide. EphA3 antigens, when
XX presented by an antigen presenting cell having a HLA class II molecule,
XX effectively induce activation and proliferation of CD4+ T lymphocytes.
XX EphA3 is a tumour associated gene. EphA3 HLA binding peptides are used
XX for selectively enriching a population of T lymphocytes. The peptides
XX are also used for diagnosing a disorder characterized by EphA3 or EphA3
XX HLA binding peptide expression. The peptides are also used to treat a
XX disorder characterized by EphA3 expression. The EphA3 binding peptides
XX are useful in producing vaccines and antibody.
XX SQ Sequence 9 AA;
Query Match 82.5%; Score 47; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
Db 2 llmwitqc 9

RESULT 15
AAB22791
ID AAB22791 standard; peptide; 9 AA.
XX AC AAB22791;
XX DT 22-DEC-2000 (first entry)
XX DE NY-ESO-1 peptide epitope, SEQ ID NO:2.
XX KW NY-ESO-1; epitope; CTL response; cytotoxic T lymphocyte; vaccine;
```


KW immunogenic; adjuvant coadministration; microbial infection;
KW tuberculosis; HIV; hepatitis B virus; hepatitis C virus; cancer.
XX
OS Unidentified.
XX
PN WO200048630-A1.
XX
PD 24-AUG-2000.
XX
PF 17-FEB-2000; 2000WO-AU00110.
XX
PR 17-FEB-1999; 99AU-0008735.
PR 27-JUL-1999; 99AU-0001861.
XX
PA (CSLC-) CSL LTD.
XX
PI Cox JC, Drane DP;
XX
DR WPI; 2000-571930/53.
XX
PT Immunogenic complexes comprising negatively charged organic carrier
PT adjuvants and positively charged antigens for use as vaccines against
PT microbial infection and cancer
XX
PS Example 4; Fig 5c; 111pp; English.
XX
CC The invention relates to a novel immunogenic complex comprising a
CC charged organic carrier and a charged antigen which are
CC electrostatically associated. The complex induces a cytotoxic T
CC lymphocyte (CTL) response. The complex and/or vaccine can be used to
CC treat a disease in a mammal, where the complex/vaccine elicits, induces
CC or otherwise facilitates an immune response which inhibits, halts, delays
CC or prevents the onset or progression of the disease condition. In
CC particular, the disease is a condition resulting from a microbial
CC infection or cancer. Microbial infections which may be treated using the
CC immunogenic complex include human immunodeficiency virus (HIV), hepatitis
CC B, hepatitis C, tuberculosis or a parasitic condition, and cancers which
CC may be treated include melanoma, prostate cancer or breast cancer. The
CC complexes and vaccines simultaneously co-deliver antigen and adjuvant to
CC the same antigen presenting cell, which is often essential for induction
CC of appropriate immune responses. Sequences AAB22790-B22791 represent
CC peptide epitopes of the positively charged protein NY-ESO-1 used in an
CC exemplification of the invention.
XX
SQ Sequence 9 AA;

Query Match 82.5%; Score 47; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
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Db 2 llmwitqc 9

Search completed: July 16, 2002, 08:01:30
Job time: 783 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	57	100.0	10	15 US-09-165-546A-7	Sequence 7, Appli
2	57	100.0	10	19 US-09-529-206-92	Sequence 92, Appl
3	57	100.0	10	19 US-09-529-206A-92	Sequence 92, Appl
4	57	100.0	10	19 US-09-529-206B-92	Sequence 92, Appl
5	53	93.0	9	18 US-09-409-455A-123	Sequence 123, App
6	53	93.0	9	19 US-09-529-206-71	Sequence 71, Appl
7	53	93.0	9	19 US-09-529-206-72	Sequence 72, Appl

8	53	93.0	9	19	US-09-529-206A-71	Sequence 71, Appl
9	53	93.0	9	19	US-09-529-206A-72	Sequence 72, Appl
10	53	93.0	9	19	US-09-529-206B-71	Sequence 71, Appl
11	53	93.0	9	19	US-09-529-206B-72	Sequence 72, Appl
12	53	93.0	9	22	US-09-833-039-123	Sequence 123, App
13	53	93.0	10	19	US-09-529-206-95	Sequence 95, Appl
14	53	93.0	10	19	US-09-529-206A-95	Sequence 95, Appl
15	53	93.0	10	19	US-09-529-206B-95	Sequence 95, Appl
16	53	93.0	10	20	US-09-676-005B-11	Sequence 11, Appl
17	47	82.5	9	1	PCT-US00-04326-43	Sequence 43, Appl
18	47	82.5	9	1	PCT-US99-06875-5	Sequence 5, Appli
19	47	82.5	9	2	US-06-670-456A-1	Sequence 1, Appli
20	47	82.5	9	15	US-09-165-546A-5	Sequence 5, Appli
21	47	82.5	9	17	US-09-336-091-42	Sequence 42, Appl
22	47	82.5	9	17	US-09-396-315-80	Sequence 80, Appl
23	47	82.5	9	18	US-09-408-036B-5	Sequence 5, Appli
24	47	82.5	9	18	US-09-440-621-2	Sequence 2, Appli
25	47	82.5	9	19	US-09-510-635A-5	Sequence 5, Appli
26	47	82.5	9	19	US-09-574-749-34	Sequence 34, Appl
27	47	82.5	9	20	US-09-676-005B-2	Sequence 2, Appli
28	47	82.5	9	20	US-09-692-401-44	Sequence 44, Appl
29	47	82.5	9	20	US-09-697-884-80	Sequence 80, Appl
30	47	82.5	9	21	US-09-705-160-43	Sequence 43, Appl
31	47	82.5	9	21	US-09-751-798-5	Sequence 5, Appli
32	47	82.5	9	21	US-09-766-889A-51	Sequence 51, Appl
33	47	82.5	9	23	US-09-913-756-43	Sequence 43, Appl
34	47	82.5	9	24	US-10-023-182-5	Sequence 5, Appli
35	47	82.5	9	24	US-10-080-013-24	Sequence 24, Appl
36	47	82.5	9	26	US-60-336-968-12	Sequence 12, Appl
37	47	82.5	10	20	US-09-676-005B-13	Sequence 13, Appl
38	47	82.5	10	20	US-09-676-005B-14	Sequence 14, Appl
39	44	77.2	9	19	US-09-529-206-68	Sequence 68, Appl
40	44	77.2	9	19	US-09-529-206A-68	Sequence 68, Appl
41	44	77.2	9	19	US-09-529-206B-68	Sequence 68, Appl
42	44	77.2	10	19	US-09-529-206-94	Sequence 94, Appl
43	44	77.2	10	19	US-09-529-206A-94	Sequence 94, Appl
44	44	77.2	10	19	US-09-529-206B-94	Sequence 94, Appl
45	44	77.2	10	20	US-09-676-005B-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-165-546A-7
; Sequence 7, Application US/09165546A
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
; Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
; AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
; MHC CLASS I AND MHC CLASS II MOLECULES, AND
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546A
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998

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; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-165-546A-7

Query Match      100.0%; Score 57; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
   |||||
Db 1 LLMWITQCFL 10

RESULT 2
US-09-529-206-92
; Sequence 92, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-92

Query Match      100.0%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
   |||||
Db 1 LLMWITQCFL 10

RESULT 3
US-09-529-206A-92
; Sequence 92, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
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; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-92

Query Match      100.0%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
   |||||
Db 1 LLMWITQCFL 10

RESULT 4
US-09-529-206B-92
; Sequence 92, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-92

Query Match      100.0%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
   |||||
Db 1 LLMWITQCFL 10

RESULT 5
US-09-409-455A-123
; Sequence 123, Application US/09409455A
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622
; CURRENT APPLICATION NUMBER: US/09/409,455A
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-409-455A-123

Query Match          93.0%; Score 53; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLMWITQCFL 10
Db 1 LLMWITQCFL 9

RESULT 6
US-09-529-206-71
; Sequence 71, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-71

Query Match          93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLMWITQCFL 10
Db 1 LLMWITQCFL 9

RESULT 7
US-09-529-206-72
; Sequence 72, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-72

Query Match          93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
Db 1 LLMWITQCF 9
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RESULT 8
US-09-529-206A-71
; Sequence 71, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-71

Query Match          93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLMWITQCFL 10
Db 1 LLMWITQCFL 9

RESULT 9
US-09-529-206A-72
; Sequence 72, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206A-72

Query Match          93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
Db 1 LLMWITQCF 9

RESULT 10
US-09-529-206B-71
; Sequence 71, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
```

; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-71

Query Match 93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLMWITQCF 10
| | | | | | | |
Db 1 LLMWITQCF 9

RESULT 11
US-09-529-206B-72
; Sequence 72, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-72

Query Match 93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
| | | | | | | |
Db 1 LLMWITQCF 9

RESULT 12
US-09-833-039-123
; Sequence 123, Application US/09833039
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/344,040

; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039-123

Query Match 93.0%; Score 53; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLMWITQCF 10
| | | | | | | |
Db 1 LLMWITQCF 9

RESULT 13
US-09-529-206-95
; Sequence 95, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206-95

Query Match 93.0%; Score 53; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
| | | | | | | |
Db 2 LLMWITQCF 10

RESULT 14
US-09-529-206A-95
; Sequence 95, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-529-206A-95

Query Match 93.0%; Score 53; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9
|
Db 2 LLMWITQCF 10

RESULT 15
US-09-529-206B-95
; Sequence 95, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-95

Query Match 93.0%; Score 53; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9
|
Db 2 LLMWITQCF 10

Search completed: July 16, 2002, 08:04:54
Job time: 242 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 08:00:02 ; Search time 16.99 Seconds
(without alignments)
65.466 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 344541 seqs, 111227333 residues

Total number of hits satisfying chosen parameters: 37342

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	53	93.0	9	5	US-09-344-040C-123
2	53	93.0	9	6	US-10-177-277-123
3	47	82.5	9	1	PCT-US02-05748-24
4	47	82.5	9	5	US-09-344-040C-131
5	47	82.5	9	5	US-09-670-456A-1
6	47	82.5	9	5	US-09-574-749B-34
7	47	82.5	9	6	US-10-117-937-197
8	47	82.5	9	6	US-10-177-277-131
9	44	77.2	9	6	US-10-117-937-196
10	38	66.7	9	1	PCT-US02-05748-25
11	33	57.9	9	1	PCT-US02-05748-26
12	33	57.9	9	5	US-09-344-040C-122
13	33	57.9	9	5	US-09-344-040C-132
14	33	57.9	9	5	US-09-574-749B-35
15	33	57.9	9	6	US-10-177-277-122
16	33	57.9	9	6	US-10-177-277-132
17	33	57.9	10	5	US-09-344-040C-129
18	33	57.9	10	6	US-10-117-937-203
19	33	57.9	10	6	US-10-177-277-129
20	30	52.6	9	5	US-09-595-334C-638
21	30	52.6	9	5	US-09-602-016C-638
22	30	52.6	9	5	US-09-570-582C-797
23	30	52.6	9	5	US-09-602-152C-638
24	30	52.6	9	5	US-09-621-630B-638
25	30	52.6	10	6	US-10-105-299-3789
26	29	50.9	9	6	US-10-117-937-202

27	28	49.1	9	6	US-10-117-937-199	Sequence 199, App
28	27	47.4	7	6	US-10-083-894-9	Sequence 9, Appli
29	23	40.4	8	5	US-09-722-250-259	Sequence 259, App
30	23	40.4	8	5	US-09-722-250-259	Sequence 259, App
31	23	40.4	9	5	US-09-722-250-374	Sequence 374, App
32	23	40.4	9	5	US-09-722-250-374	Sequence 374, App
33	22	38.6	4	5	US-09-573-655B-2844	Sequence 2844, Ap
34	22	38.6	4	5	US-09-692-714A-349	Sequence 349, App
35	22	38.6	4	5	US-09-692-717A-349	Sequence 349, App
36	22	38.6	4	5	US-09-620-393B-9512	Sequence 9512, Ap
37	22	38.6	4	5	US-09-696-751-349	Sequence 349, App
38	22	38.6	4	5	US-09-935-625-32674	Sequence 32674, A
39	22	38.6	7	5	US-09-722-250-287	Sequence 287, App
40	22	38.6	7	5	US-09-722-250-287	Sequence 287, App
41	22	38.6	8	5	US-09-595-334C-459	Sequence 459, App
42	22	38.6	8	5	US-09-602-016C-459	Sequence 459, App
43	22	38.6	8	5	US-09-573-655B-3020	Sequence 3020, Ap
44	22	38.6	8	5	US-09-587-811A-5	Sequence 5, Appli
45	22	38.6	8	5	US-09-570-582C-618	Sequence 618, App

ALIGNMENTS

RESULT 1
US-09-344-040C-123
; Sequence 123, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Deter
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gen
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-123

Query Match 93.0%; Score 53; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.le+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMWITQCFL 10
Db 1 LMWITQCFL 9

RESULT 2
US-10-177-277-123
; Sequence 123, Application US/10177277
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Deter
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gen
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1

;
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-123

Query Match 93.0%; Score 53; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLMWITQCFL 10
| | | | | | | |
Db 1 LLMWITQCFL 9

RESULT 3
PCT-US02-05748-24
; Sequence 24, Application PC/TUS0205748
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Leturcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: PCT/US02/05748
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-05748-24

Query Match 82.5%; Score 47; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
| | | | | | | |
Db 2 LLMWITQC 9

RESULT 4
US-09-344-040C-131
; Sequence 131, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839

;
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 131
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-131

Query Match 82.5%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
| | | | | | | |
Db 2 LLMWITQC 9

RESULT 5
US-09-670-456A-1
; Sequence 1, Application US/09670456A
; GENERAL INFORMATION:
; LUD-5668-PCT
; APPLICANT: Gnjatich, Sacha
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA-C MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: LUD 5668
; CURRENT APPLICATION NUMBER: US/09/670,456A
; CURRENT FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-670-456A-1

Query Match 82.5%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
| | | | | | | |
Db 2 LLMWITQC 9

RESULT 6
US-09-574-749B-34
; Sequence 34, Application US/09574749B
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; TITLE OF INVENTION: DEVICES
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/09/574,749B
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 9

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-09-574-749B-34

Query Match 82.5%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
| | | | | | | |
Db 2 LLMWITQC 9

RESULT 7

US-10-117-937-197
; Sequence 197, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPI TOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 197
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-197

Query Match 82.5%; Score 47; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
| | | | | | | |
Db 2 LLMWITQC 9

RESULT 8

US-10-177-277-131
; Sequence 131, Application US/10177277
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130

; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 131
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-131

Query Match 82.5%; Score 47; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
| | | | | | | |
Db 2 LLMWITQC 9

RESULT 9

US-10-117-937-196
; Sequence 196, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPI TOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-196

Query Match 77.2%; Score 44; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 WITQCFL 10
| | | | | | | |
Db 1 WITQCFL 7

RESULT 10

PCT-US02-05748-25
; Sequence 25, Application PC/TUS0205748
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Leturcq, Juli
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: PCT/US02/05748
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 9

; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-05748-25

Query Match 66.7%; Score 38; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQ 7
| | | | | | |
Db 2 LLMWITQ 8

RESULT 11
PCT-US02-05748-26
; Sequence 26, Application PC/TUS0205748
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Leturcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: PCT/US02/05748
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-05748-26

Query Match 57.9%; Score 33; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
| | | | | | |
Db 4 LLMWIT 9

RESULT 12
US-09-344-040C-122
; Sequence 122, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Presence of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 122
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-122

Query Match 57.9%; Score 33; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
| | | | | | |
Db 4 LLMWIT 9

RESULT 13
US-09-344-040C-132
; Sequence 132, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Presence of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-132

Query Match 57.9%; Score 33; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
| | | | | | |
Db 4 LLMWIT 9

RESULT 14
US-09-574-749B-35
; Sequence 35, Application US/09574749B
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/09/574,749B
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source

US-09-574-749B-35

Query Match 57.9%; Score 33; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
Db 4 LLMWIT 9

RESULT 15
US-10-177-277-122
; Sequence 122, Application US/10177277
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 122
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-122

Query Match 57.9%; Score 33; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
Db 4 LLMWIT 9

Search completed: July 16, 2002, 08:03:20
Job time: 198 sec

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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:56:42 ; Search time 15.68 Seconds
(without alignments)
15.578 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 70601

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	57	100.0	10	4	US-09-359-503-7
2	47	82.5	9	4	US-09-183-931-43
3	47	82.5	9	4	US-09-359-503-5
4	47	82.5	9	4	US-09-062-422-5
5	47	82.5	9	4	US-08-937-263B-5
6	47	82.5	9	4	US-09-166-448-80
7	33	57.9	6	4	US-09-359-503-14
8	33	57.9	6	4	US-09-062-422-7
9	33	57.9	6	4	US-08-937-263B-7
10	33	57.9	9	4	US-09-183-931-44
11	33	57.9	9	4	US-09-359-503-6
12	33	57.9	9	4	US-09-062-422-6
13	33	57.9	9	4	US-08-937-263B-6
14	33	57.9	9	4	US-09-166-448-81
15	27	47.4	8	4	US-09-020-065A-24
16	26	45.6	6	2	US-08-482-228-186
17	26	45.6	6	3	US-08-482-528-186
18	26	45.6	10	4	US-09-248-588-35
19	25	43.9	9	1	US-08-484-044-7
20	25	43.9	10	3	US-08-768-859A-15
21	25	43.9	10	3	US-08-767-820A-15
22	25	43.9	10	5	PCT-US95-06157-15
23	24	42.1	10	4	US-08-379-580-6
24	23	40.4	6	1	US-07-620-426B-2
25	23	40.4	6	1	US-07-662-007B-2
26	23	40.4	6	1	US-07-824-247-2
27	23	40.4	6	3	US-08-470-204A-2

28	23	40.4	8	4	US-09-258-754-259	Sequence 259, App
29	23	40.4	8	4	US-09-042-107-259	Sequence 259, App
30	23	40.4	9	4	US-09-258-754-374	Sequence 374, App
31	23	40.4	9	4	US-09-042-107-374	Sequence 374, App
32	23	40.4	10	2	US-08-764-640-103	Sequence 103, App
33	23	40.4	10	3	US-08-159-339A-477	Sequence 477, App
34	23	40.4	10	3	US-08-973-225-103	Sequence 103, App
35	23	40.4	10	3	US-09-244-298A-103	Sequence 103, App
36	23	40.4	10	4	US-08-378-313-11	Sequence 11, Appl
37	23	40.4	10	4	US-09-516-704-103	Sequence 103, App
38	22	38.6	6	2	US-08-621-803-182	Sequence 182, App
39	22	38.6	6	2	US-08-621-803-183	Sequence 183, App
40	22	38.6	6	2	US-08-621-259A-149	Sequence 149, App
41	22	38.6	6	4	US-09-217-352-182	Sequence 182, App
42	22	38.6	6	4	US-09-217-352-183	Sequence 183, App
43	22	38.6	6	4	US-09-344-541A-59	Sequence 59, Appl
44	22	38.6	6	5	PCT-US95-09262-149	Sequence 149, App
45	22	38.6	7	1	US-08-064-517-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-359-503-7
; Sequence 7, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid

NAME: Hanson, No. 6252052man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-062-422-5

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
Db 2 LLMWITQC 9

RESULT 5
US-08-937-263B-5
Sequence 5, Application US/08937263B
Patent No. 6274145
GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
TITLE OF INVENTION: ITSELF, AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sinn, Eric, Patent Agent
REGISTRATION NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-937-263B-5

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8

Db 2 LLMWITQC 9

RESULT 6
US-09-166-448-80
Sequence 80, Application US/09166448
Patent No. 6291430
GENERAL INFORMATION:
APPLICANT: Chau, Pascal
APPLICANT: Vantomme, Valrie
APPLICANT: Stroobant, Vincent
APPLICANT: Boon-Falleur, Thierry
APPLICANT: van der Bruggen, Pierre
APPLICANT: Thielemans, Kris
APPLICANT: Corthals, Jorgen
TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
FILE REFERENCE: L0461/7052
CURRENT APPLICATION NUMBER: US/09/166,448
CURRENT FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 80
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-166-448-80

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
Db 2 LLMWITQC 9

RESULT 7
US-09-359-503-14
Sequence 14, Application US/09359503
Patent No. 6251603
GENERAL INFORMATION:
APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263

;
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-359-503-14

Query Match 57.9%; Score 33; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
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|
|
Db 1 LLMWIT 6

RESULT 8
US-09-062-422-7
; Sequence 7, Application US/09062422
; Patent No. 6252052
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
; TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
; TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,422
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6252052man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids

;
; TYPE: amino acid
; TOPOLOGY: linear
US-09-062-422-7

Query Match 57.9%; Score 33; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
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|
|
|
Db 1 LLMWIT 6

RESULT 9
US-08-937-263B-7
; Sequence 7, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sinn, Eric, Patent Agent
REGISTRATION NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-937-263B-7

Query Match 57.9%; Score 33; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
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|
|
Db 1 LLMWIT 6

RESULT 10
US-09-183-931-44
; Sequence 44, Application US/09183931C
; Patent No. 6210886
; GENERAL INFORMATION:

; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
; FILE REFERENCE: LUD 5527.1-JEL/ES
; CURRENT APPLICATION NUMBER: US/09/183,931C
; CURRENT FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: US 09/018,422
; EARLIER FILING DATE: 1998 - 02 - 04
; . NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-183-931-44

Query Match 57.9%; Score 33; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
| | | | |
Db 4 LLMWIT 9

RESULT 11
US-09-359-503-6
; Sequence 6, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-359-503-6

Query Match 57.9%; Score 33; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
| | | | |
Db 4 LLMWIT 9

RESULT 12
US-09-062-422-6
; Sequence 6, Application US/09062422
; Patent No. 6252052
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
; TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
; TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,422
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6252052man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-062-422-6

Query Match 57.9%; Score 33; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LLMWIT 6
      |||||
Db      4 LLMWIT 9

RESULT 13
US-08-937-263B-6
; Sequence 6, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-937-263B-6

Query Match      57.9%; Score 33; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LLMWIT 6
      |||||
Db      4 LLMWIT 9

RESULT 14
US-09-166-448-81
; Sequence 81, Application US/09166448
; Patent No. 6291430
; GENERAL INFORMATION:
; APPLICANT: Chau, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgen
; TITLE OF INVENTION: MAG-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
```

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; CURRENT APPLICATION NUMBER: US/09/166,448
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-448-81

Query Match      57.9%; Score 33; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LLMWIT 6
      |||||
Db      4 LLMWIT 9

RESULT 15
US-09-020-065A-24
; Sequence 24, Application US/09020065A
; Patent No. 6346602
; GENERAL INFORMATION:
; APPLICANT: Townsend, Robert M.
; APPLICANT: Korngold, Robert
; TITLE OF INVENTION: Peptide Mimics of the Cytokine Receptor Common
; TITLE OF INVENTION: Gamma Chain and Methods and Compositions for
; TITLE OF INVENTION: Making and Using the Same
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6346602ris LLP
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Wordperfect V. 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,065A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,941
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-2291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-09-020-065A-24

Query Match      47.4%; Score 27; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 LMWITQC 8
      | : |||
Db      2 LQYLTQC 8
```

Search completed: July 16, 2002, 08:02:06
Job time: 324 sec